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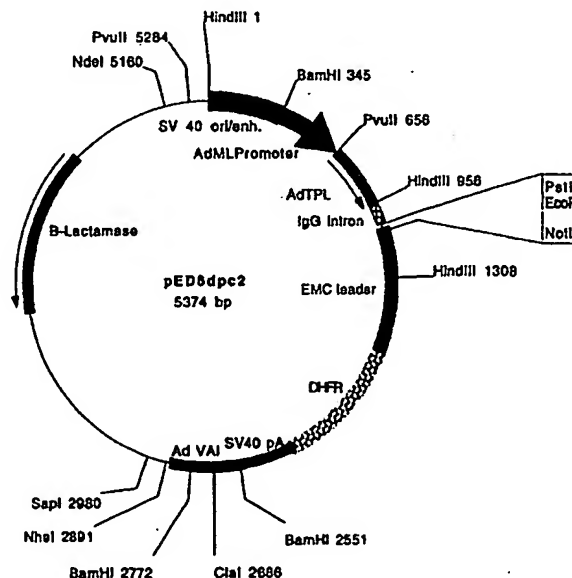
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(54) Title: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM

(57) Abstract

Novel polynucleotides and the proteins encoded thereby are disclosed.



Plasmid name: pED8dpc2
Plasmid size: 5374 bp

Comments/References: pED8dpc2 is derived from pED8dpc1 by insertion of a new polylinker to facilitate cDNA cloning. SST cDNAs are cloned between EcoRI and NotI. pED vectors are described in Kautman et al.(1991), NAR 19: 4485-4490.

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SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM

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This application is a continuation-in-part of the following applications:

- 15 (1) provisional application Ser. No. 60/075,118, filed February 11, 1998, now abandoned;
- (2) application Ser. No. 09/248,059, filed February 10, 1999; which is a continuation-in-part of provisional application Ser. No. 60/075,118, filed February 11, 1998, now abandoned;
- 20 (3) provisional application Ser. No. 60/080,969, filed April 7, 1998, now abandoned;
- (4) application Ser. No. 09/287,150, filed April 6, 1999; which is a continuation-in-part of provisional application Ser. No. 60/080,969, filed April 7, 1998, now abandoned;
- (5) provisional application Ser. No. 60/085,472, filed May 14, 1998;
- 25 (6) provisional application Ser. No. 60/096,824, filed August 17, 1998;
- (7) provisional application Ser. No. 60/099,950, filed September 11, 1998;
- (8) provisional application Ser. No. 60/099,843, filed September 11, 1998;
- (9) provisional application Ser. No. 60/100,424, filed September 15, 1998;
- (10) provisional application Ser. No. 60/102,329, filed September 29, 1998;
- (11) provisional application Ser. No. 60/103,615, filed October 9, 1998;
- 30 (12) provisional application Ser. No. 60/111,799, filed December 11, 1998;
- (13) provisional application Ser. No. 60/112,159, filed December 14, 1998;
- (14) provisional application Ser. No. 60/114,415, filed December 31, 1998;
- all of which are incorporated by reference herein.

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FIELD OF THE INVENTION

The present invention provides novel polynucleotides and proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these
10 polynucleotides and proteins.

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BACKGROUND OF THE INVENTION

Technology aimed at the discovery of protein factors (including e.g., cytokines, such as lymphokines, interferons, CSFs and interleukins) has matured rapidly over the past decade. The now routine hybridization cloning and expression cloning techniques clone novel polynucleotides "directly" in the sense that they rely on information directly
20 related to the discovered protein (i.e., partial DNA/amino acid sequence of the protein in the case of hybridization cloning; activity of the protein in the case of expression cloning). More recent "indirect" cloning techniques such as signal sequence cloning, which isolates DNA sequences based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization cloning
25 techniques, have advanced the state of the art by making available large numbers of DNA/amino acid sequences for proteins that are known to have biological activity by virtue of their secreted nature in the case of leader sequence cloning, or by virtue of the cell or tissue source in the case of PCR-based techniques. It is to these proteins and the polynucleotides encoding them that the present invention is directed.

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SUMMARY OF THE INVENTION

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide 29 to nucleotide 253;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ya15_1 deposited under accession number
10 ATCC 98650;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ya15_1 deposited under accession number ATCC 98650;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ya15_1 deposited under accession number ATCC
15 98650;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ya15_1 deposited under accession number ATCC 98650;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:2;
- 20 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:2;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- 25 (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:1.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:1 from nucleotide 29 to nucleotide 253; the nucleotide sequence of the full-length protein coding sequence of clone ya15_1 deposited under accession number ATCC 98650;

or the nucleotide sequence of a mature protein coding sequence of clone ya15_1 deposited under accession number ATCC 98650. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ya15_1 deposited under accession number ATCC 98650. In further preferred
5 embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:2, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having
10 biological activity, the fragment comprising the amino acid sequence from amino acid 32 to amino acid 41 of SEQ ID NO:2.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:1.

Further embodiments of the invention provide isolated polynucleotides produced
15 according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

20 (aa) SEQ ID NO:1, but excluding the poly(A) tail at the 3' end of SEQ ID NO:1; and

(ab) the nucleotide sequence of the cDNA insert of clone ya15_1 deposited under accession number ATCC 98650;

25 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that
30 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:1, but excluding the poly(A) tail at the 3' end of SEQ ID NO:1; and

- (bb) the nucleotide sequence of the cDNA insert of clone ya15_1 deposited under accession number ATCC 98650;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 5 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:1, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:1 to

10 a nucleotide sequence corresponding to the 3' end of SEQ ID NO:1, but excluding the poly(A) tail at the 3' end of SEQ ID NO:1. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:1 from nucleotide 29 to nucleotide 253, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of

15 SEQ ID NO:1 from nucleotide 29 to nucleotide 253, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:1 from nucleotide 29 to nucleotide 253.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group

20 consisting of:

- (a) the amino acid sequence of SEQ ID NO:2;
- (b) a fragment of the amino acid sequence of SEQ ID NO:2, the fragment comprising eight contiguous amino acids of SEQ ID NO:2; and
- (c) the amino acid sequence encoded by the cDNA insert of clone
- 25 ya15_1 deposited under accession number ATCC 98650;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:2. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment preferably

30 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:2, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment comprising the amino acid sequence from amino acid 32 to amino acid 41 of SEQ ID NO:2.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:3;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:3 from nucleotide 151 to nucleotide 288;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:3 from nucleotide 196 to nucleotide 288;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ya24_1 deposited under accession number
10 ATCC 98650;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ya24_1 deposited under accession number ATCC 98650;
- (f) a polynucleotide comprising the nucleotide sequence of a mature
15 protein coding sequence of clone ya24_1 deposited under accession number ATCC 98650;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ya24_1 deposited under accession number ATCC 98650;
- (h) a polynucleotide encoding a protein comprising the amino acid
20 sequence of SEQ ID NO:4;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:4;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of
25 (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 30 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:3.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:3 from nucleotide 151 to nucleotide 288; the nucleotide sequence of SEQ ID NO:3 from

nucleotide 196 to nucleotide 288; the nucleotide sequence of the full-length protein coding sequence of clone ya24_1 deposited under accession number ATCC 98650; or the nucleotide sequence of a mature protein coding sequence of clone ya24_1 deposited under accession number ATCC 98650. In other preferred embodiments, the polynucleotide
5 encodes the full-length or a mature protein encoded by the cDNA insert of clone ya24_1 deposited under accession number ATCC 98650. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous
10 amino acids of SEQ ID NO:4, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment comprising the amino acid sequence from amino acid 18 to amino acid 27 of SEQ ID NO:4.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ
15 ID NO:3.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize
20 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:3, but excluding the poly(A) tail at the 3' end of SEQ ID NO:3; and
 - (ab) the nucleotide sequence of the cDNA insert of clone
25 ya24_1 deposited under accession number ATCC 98650;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);
30
- and
- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:3, but excluding the poly(A) tail at the 3' end of SEQ ID NO:3; and

(bb) the nucleotide sequence of the cDNA insert of clone ya24_1 deposited under accession number ATCC 98650;

5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a
10 nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:3, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:3 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:3, but excluding the poly(A) tail at the 3' end of SEQ ID NO:3. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the
15 cDNA sequence of SEQ ID NO:3 from nucleotide 151 to nucleotide 288, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:3 from nucleotide 151 to nucleotide 288, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:3 from nucleotide 151 to nucleotide 288. Also preferably the polynucleotide isolated according to the above
20 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:3 from nucleotide 196 to nucleotide 288, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:3 from nucleotide 196 to nucleotide 288, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:3 from nucleotide 196 to nucleotide 288.

25 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:4;

(b) a fragment of the amino acid sequence of SEQ ID NO:4, the
30 fragment comprising eight contiguous amino acids of SEQ ID NO:4; and

(c) the amino acid sequence encoded by the cDNA insert of clone ya24_1 deposited under accession number ATCC 98650;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:4. In further preferred

embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:4, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment comprising the amino acid sequence from amino acid 18 to amino acid 27 of SEQ ID NO:4.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 10 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:5;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:5 from nucleotide 615 to nucleotide 908;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:5 from nucleotide 774 to nucleotide 908;
- 15 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yb42_1 deposited under accession number ATCC 98650;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yb42_1 deposited under accession number ATCC 98650;
- 20 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yb42_1 deposited under accession number ATCC 98650;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yb42_1 deposited under accession number ATCC 98650;
- 25 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:6;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:6;
- 30 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:5.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:5 from nucleotide 615 to nucleotide 908; the nucleotide sequence of SEQ ID NO:5 from nucleotide 774 to nucleotide 908; the nucleotide sequence of the full-length protein coding sequence of clone yb42_1 deposited under accession number ATCC 98650; or the nucleotide sequence of a mature protein coding sequence of clone yb42_1 deposited under accession number ATCC 98650. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yb42_1 deposited under accession number ATCC 98650. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:6, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment comprising the amino acid sequence from amino acid 44 to amino acid 53 of SEQ ID NO:6.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:5.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:5, but excluding the poly(A) tail at the 3' end of SEQ ID NO:5; and
 - (ab) the nucleotide sequence of the cDNA insert of clone yb42_1 deposited under accession number ATCC 98650;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

5 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:5, but excluding the poly(A) tail at the 3' end of SEQ ID NO:5; and

10 (bb) the nucleotide sequence of the cDNA insert of clone yb42_1 deposited under accession number ATCC 98650;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

15 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:5, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:5 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:5, but excluding the poly(A) tail at the 3' end of SEQ ID NO:5. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:5 from nucleotide 615 to nucleotide 908, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:5 from nucleotide 615 to nucleotide 908, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:5 from nucleotide 615 to nucleotide 908. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:5 from nucleotide 774 to nucleotide 908, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:5 from nucleotide 774 to nucleotide 908, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:5 from nucleotide 774 to nucleotide 908.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:6;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:6, the fragment comprising eight contiguous amino acids of SEQ ID NO:6; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone yb42_1 deposited under accession number ATCC 98650;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:6. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:6, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment comprising the amino acid sequence from amino acid 44 to amino acid 53 of SEQ ID NO:6.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7 from nucleotide 1203 to nucleotide 2327;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yc9_1 deposited under accession number ATCC 98650;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yc9_1 deposited under accession number ATCC 98650;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yc9_1 deposited under accession number ATCC 98650;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yc9_1 deposited under accession number ATCC 98650;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:8;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:8;

- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- 5 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:7.
- 10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:7 from nucleotide 1203 to nucleotide 2327; the nucleotide sequence of the full-length protein coding sequence of clone yc9_1 deposited under accession number ATCC 98650; or the nucleotide sequence of a mature protein coding sequence of clone yc9_1 deposited under accession number ATCC 98650. In other preferred embodiments, the
- 15 polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yc9_1 deposited under accession number ATCC 98650. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment preferably comprising eight (more preferably twenty, most
- 20 preferably thirty) contiguous amino acids of SEQ ID NO:8, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment comprising the amino acid sequence from amino acid 182 to amino acid 191 of SEQ ID NO:8.
- Other embodiments provide the gene corresponding to the cDNA sequence of SEQ
- 25 ID NO:7.
- Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:
- (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize
- 30 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (aa) SEQ ID NO:7, but excluding the poly(A) tail at the 3' end of SEQ ID NO:7; and

- (ab) the nucleotide sequence of the cDNA insert of clone yc9_1 deposited under accession number ATCC 98650;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 5 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 10 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:7, but excluding the poly(A) tail at the 3' end of SEQ ID NO:7; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 15 yc9_1 deposited under accession number ATCC 98650;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- 20 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:7, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:7 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:7, but excluding the poly(A) tail at the 3' end of SEQ ID NO:7. Also preferably the polynucleotide isolated
- 25 according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:7 from nucleotide 1203 to nucleotide 2327, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:7 from nucleotide 1203 to nucleotide 2327, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:7 from nucleotide 1203 to
- 30 nucleotide 2327.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:8;

- (b) a fragment of the amino acid sequence of SEQ ID NO:8, the fragment comprising eight contiguous amino acids of SEQ ID NO:8; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yc9_1 deposited under accession number ATCC 98650;
- 5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:8. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 10 of SEQ ID NO:8, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment comprising the amino acid sequence from amino acid 182 to amino acid 191 of SEQ ID NO:8.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9 from nucleotide 230 to nucleotide 823;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
- 20 NO:9 from nucleotide 584 to nucleotide 823;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yc19_1 deposited under accession number ATCC 98650;
- (e) a polynucleotide encoding the full-length protein encoded by the
- 25 cDNA insert of clone yc19_1 deposited under accession number ATCC 98650;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yc19_1 deposited under accession number ATCC 98650;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA
- 30 insert of clone yc19_1 deposited under accession number ATCC 98650;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:10;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:10;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:9.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:9 from nucleotide 230 to nucleotide 823; the nucleotide sequence of SEQ ID NO:9 from nucleotide 584 to nucleotide 823; the nucleotide sequence of the full-length protein coding sequence of clone yc19_1 deposited under accession number ATCC 98650; or the nucleotide sequence of a mature protein coding sequence of clone yc19_1 deposited under accession number ATCC 98650. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yc19_1 deposited under accession number ATCC 98650. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:10, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment comprising the amino acid sequence from amino acid 94 to amino acid 103 of SEQ ID NO:10.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:9.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- 5 (aa) SEQ ID NO:9, but excluding the poly(A) tail at the 3' end of SEQ ID NO:9; and
- (ab) the nucleotide sequence of the cDNA insert of clone yc19_1 deposited under accession number ATCC 98650;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 10 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 15 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:9, but excluding the poly(A) tail at the 3' end of SEQ ID NO:9; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 20 yc19_1 deposited under accession number ATCC 98650;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- 25 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:9, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:9 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:9, but excluding the poly(A) tail at the 3' end of SEQ ID NO:9. Also preferably the polynucleotide isolated
- 30 according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:9 from nucleotide 230 to nucleotide 823, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:9 from nucleotide 230 to nucleotide 823, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:9 from nucleotide 230 to

nucleotide 823. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:9 from nucleotide 584 to nucleotide 823, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:9 from nucleotide 584 to nucleotide 823, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:9 from nucleotide 584 to nucleotide 823.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:10;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:10, the fragment comprising eight contiguous amino acids of SEQ ID NO:10; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone yc19_1 deposited under accession number ATCC 98650;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:10. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 20 of SEQ ID NO:10, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment comprising the amino acid sequence from amino acid 94 to amino acid 103 of SEQ ID NO:10.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:11;
 - (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:11 from nucleotide 292 to nucleotide 534;
 - (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yc20_1 deposited under accession number
- 30 ATCC 98650;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yc20_1 deposited under accession number ATCC 98650;

- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yc20_1 deposited under accession number ATCC 98650;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yc20_1 deposited under accession number ATCC 98650;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:12;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:12;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:11.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:11 from nucleotide 292 to nucleotide 534; the nucleotide sequence of the full-length protein coding sequence of clone yc20_1 deposited under accession number ATCC 98650; or the nucleotide sequence of a mature protein coding sequence of clone yc20_1 deposited under accession number ATCC 98650. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yc20_1 deposited under accession number ATCC 98650. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:12, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment comprising the amino acid sequence from amino acid 35 to amino acid 44 of SEQ ID NO:12.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:11.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 5 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - 10 (aa) SEQ ID NO:11, but excluding the poly(A) tail at the 3' end of SEQ ID NO:11; and
 - (ab) the nucleotide sequence of the cDNA insert of clone yc20_1 deposited under accession number ATCC 98650;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - 15 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
 - 20 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (ba) SEQ ID NO:11, but excluding the poly(A) tail at the 3' end of SEQ ID NO:11; and
 - (bb) the nucleotide sequence of the cDNA insert of clone
 - 25 yc20_1 deposited under accession number ATCC 98650;
 - (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
 - (iii) amplifying human DNA sequences; and
 - (iv) isolating the polynucleotide products of step (b)(iii).
- 30 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:11, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:11 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:11, but excluding the poly(A) tail at the 3' end of SEQ ID NO:11. Also preferably the

polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:11 from nucleotide 292 to nucleotide 534, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:11 from nucleotide 292 to nucleotide 534, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:11 from nucleotide 292 to nucleotide 534.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:12;
- (b) a fragment of the amino acid sequence of SEQ ID NO:12, the fragment comprising eight contiguous amino acids of SEQ ID NO:12; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yc20_1 deposited under accession number ATCC 98650;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:12. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 20 of SEQ ID NO:12, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment comprising the amino acid sequence from amino acid 35 to amino acid 44 of SEQ ID NO:12.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:13;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:13 from nucleotide 45 to nucleotide 590;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:13 from nucleotide 126 to nucleotide 590;
- 30 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ya9_1 deposited under accession number ATCC 98724;

- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ya9_1 deposited under accession number ATCC 98724;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ya9_1 deposited under accession number ATCC 98724;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ya9_1 deposited under accession number ATCC 98724;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:14;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:14;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:13.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:13 from nucleotide 45 to nucleotide 590; the nucleotide sequence of SEQ ID NO:13 from nucleotide 126 to nucleotide 590; the nucleotide sequence of the full-length protein coding sequence of clone ya9_1 deposited under accession number ATCC 98724; or the nucleotide sequence of a mature protein coding sequence of clone ya9_1 deposited under accession number ATCC 98724. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ya9_1 deposited under accession number ATCC 98724. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:14, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the

fragment comprising the amino acid sequence from amino acid 86 to amino acid 95 of SEQ ID NO:14.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:13.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group
10 consisting of:

(aa) SEQ ID NO:13, but excluding the poly(A) tail at the 3' end of SEQ ID NO:13; and

(ab) the nucleotide sequence of the cDNA insert of clone ya9_1 deposited under accession number ATCC 98724;

15 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25 (ba) SEQ ID NO:13, but excluding the poly(A) tail at the 3' end of SEQ ID NO:13; and

(bb) the nucleotide sequence of the cDNA insert of clone ya9_1 deposited under accession number ATCC 98724;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

30 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:13, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

ID NO:13 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:13, but excluding the poly(A) tail at the 3' end of SEQ ID NO:13. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:13 from nucleotide 45 to nucleotide 590, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:13 from nucleotide 45 to nucleotide 590, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:13 from nucleotide 45 to nucleotide 590. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:13 from nucleotide 126 to nucleotide 590, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:13 from nucleotide 126 to nucleotide 590, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:13 from nucleotide 126 to nucleotide 590.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:14;
- (b) a fragment of the amino acid sequence of SEQ ID NO:14, the fragment comprising eight contiguous amino acids of SEQ ID NO:14; and
- (c) the amino acid sequence encoded by the cDNA insert of clone ya9_1 deposited under accession number ATCC 98724;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:14. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:14, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment comprising the amino acid sequence from amino acid 86 to amino acid 95 of SEQ ID NO:14.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:15;

- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:15 from nucleotide 194 to nucleotide 466;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:15 from nucleotide 338 to nucleotide 466;
- 5 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ya11_1 deposited under accession number ATCC 98724;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ya11_1 deposited under accession number ATCC 98724;
- 10 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ya11_1 deposited under accession number ATCC 98724;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ya11_1 deposited under accession number ATCC 98724;
- 15 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:16;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:16;
- 20 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 25 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:15.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:15 from nucleotide 194 to nucleotide 466; the nucleotide sequence of SEQ ID NO:15 from nucleotide 338 to nucleotide 466; the nucleotide sequence of the full-length protein coding sequence of clone ya11_1 deposited under accession number ATCC 98724; or the nucleotide sequence of a mature protein coding sequence of clone ya11_1 deposited under accession number ATCC 98724. In other preferred embodiments, the polynucleotide

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encodes the full-length or a mature protein encoded by the cDNA insert of clone ya11_1 deposited under accession number ATCC 98724. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:16, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment comprising the amino acid sequence from amino acid 40 to amino acid 49 of SEQ ID NO:16.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:15.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:15, but excluding the poly(A) tail at the 3' end of SEQ ID NO:15; and
 - (ab) the nucleotide sequence of the cDNA insert of clone ya11_1 deposited under accession number ATCC 98724;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (ba) SEQ ID NO:15, but excluding the poly(A) tail at the 3' end of SEQ ID NO:15; and
 - (bb) the nucleotide sequence of the cDNA insert of clone ya11_1 deposited under accession number ATCC 98724;

- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
 - (iii) amplifying human DNA sequences; and
 - (iv) isolating the polynucleotide products of step (b)(iii).
- 5 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:15, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:15 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:15, but excluding the poly(A) tail at the 3' end of SEQ ID NO:15. Also preferably the
- 10 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:15 from nucleotide 194 to nucleotide 466, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:15 from nucleotide 194 to nucleotide 466, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:15 from nucleotide
- 15 194 to nucleotide 466. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:15 from nucleotide 338 to nucleotide 466, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:15 from nucleotide 338 to nucleotide 466, to a nucleotide sequence corresponding to the 3' end of
- 20 said sequence of SEQ ID NO:15 from nucleotide 338 to nucleotide 466.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:16;
- 25 (b) a fragment of the amino acid sequence of SEQ ID NO:16, the fragment comprising eight contiguous amino acids of SEQ ID NO:16; and
- (c) the amino acid sequence encoded by the cDNA insert of clone ya11_1 deposited under accession number ATCC 98724;

the protein being substantially free from other mammalian proteins. Preferably such

30 protein comprises the amino acid sequence of SEQ ID NO:16. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:16, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:16 having biological activity, the fragment comprising the amino acid sequence from amino acid 40 to amino acid 49 of SEQ ID NO:16.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:17;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:17 from nucleotide 15 to nucleotide 233;
- 10 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:17 from nucleotide 174 to nucleotide 233;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ya28_1 deposited under accession number ATCC 98724;
- 15 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ya28_1 deposited under accession number ATCC 98724;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ya28_1 deposited under accession number ATCC 98724;
- 20 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ya28_1 deposited under accession number ATCC 98724;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:18;
- 25 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:18;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:17.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:17 from nucleotide 15 to nucleotide 233; the nucleotide sequence of SEQ ID NO:17 from nucleotide 174 to nucleotide 233; the nucleotide sequence of the full-length protein coding sequence of clone ya28_1 deposited under accession number ATCC 98724; or the
5 nucleotide sequence of a mature protein coding sequence of clone ya28_1 deposited under accession number ATCC 98724. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ya28_1 deposited under accession number ATCC 98724. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment
10 of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:18, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment comprising the amino acid sequence from amino acid 31 to amino acid 40 of SEQ
15 ID NO:18.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:17.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 20 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:17, but excluding the poly(A) tail at the
25 3' end of SEQ ID NO:17; and
 - (ab) the nucleotide sequence of the cDNA insert of clone ya28_1 deposited under accession number ATCC 98724;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - 30 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- 5 (ba) SEQ ID NO:17, but excluding the poly(A) tail at the 3' end of SEQ ID NO:17; and
- (bb) the nucleotide sequence of the cDNA insert of clone ya28_1 deposited under accession number ATCC 98724;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 10 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:17, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:17 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:17, but excluding the poly(A) tail at the 3' end of SEQ ID NO:17. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:17 from nucleotide 15 to nucleotide 233, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:17 from nucleotide 15 to nucleotide 233, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:17 from nucleotide 15 to nucleotide 233. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:17 from nucleotide 174 to nucleotide 233, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:17 from nucleotide 174 to nucleotide 233, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:17 from nucleotide 174 to nucleotide 233.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 30 (a) the amino acid sequence of SEQ ID NO:18;
- (b) a fragment of the amino acid sequence of SEQ ID NO:18, the fragment comprising eight contiguous amino acids of SEQ ID NO:18; and

(c) the amino acid sequence encoded by the cDNA insert of clone ya28_1 deposited under accession number ATCC 98724; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:18. In further preferred
5 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:18, or a protein comprising a fragment of the amino acid sequence of SEQ
10 ID NO:18 having biological activity, the fragment comprising the amino acid sequence from amino acid 31 to amino acid 40 of SEQ ID NO:18.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:19;
- 15 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:19 from nucleotide 102 to nucleotide 461;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yb81_1 deposited under accession number ATCC 98724;
- 20 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yb81_1 deposited under accession number ATCC 98724;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yb81_1 deposited under accession number ATCC 98724;
- 25 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yb81_1 deposited under accession number ATCC 98724;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:20;
- (h) a polynucleotide encoding a protein comprising a fragment of the
30 amino acid sequence of SEQ ID NO:20 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:20;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

5 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:19.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:19 from nucleotide 102 to nucleotide 461; the nucleotide sequence of the full-length
10 protein coding sequence of clone yb81_1 deposited under accession number ATCC 98724; or the nucleotide sequence of a mature protein coding sequence of clone yb81_1 deposited under accession number ATCC 98724. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yb81_1 deposited under accession number ATCC 98724. In further preferred
15 embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:20, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having
20 biological activity, the fragment comprising the amino acid sequence from amino acid 55 to amino acid 64 of SEQ ID NO:20.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:19.

Further embodiments of the invention provide isolated polynucleotides produced
25 according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

30 (aa) SEQ ID NO:19, but excluding the poly(A) tail at the 3' end of SEQ ID NO:19; and

(ab) the nucleotide sequence of the cDNA insert of clone yb81_1 deposited under accession number ATCC 98724;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

5 and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (ba) SEQ ID NO:19, but excluding the poly(A) tail at the 3' end of SEQ ID NO:19; and

(bb) the nucleotide sequence of the cDNA insert of clone yb81_1 deposited under accession number ATCC 98724;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

15 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:19, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:19 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:19, but excluding the poly(A) tail at the 3' end of SEQ ID NO:19. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:19 from nucleotide 102 to nucleotide 25 461, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:19 from nucleotide 102 to nucleotide 461, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:19 from nucleotide 102 to nucleotide 461.

30 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:20;

(b) a fragment of the amino acid sequence of SEQ ID NO:20, the fragment comprising eight contiguous amino acids of SEQ ID NO:20; and

(c) the amino acid sequence encoded by the cDNA insert of clone yb81_1 deposited under accession number ATCC 98724;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:20. In further preferred
5 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:20, or a protein comprising a fragment of the amino acid sequence of SEQ
10 ID NO:20 having biological activity, the fragment comprising the amino acid sequence from amino acid 55 to amino acid 64 of SEQ ID NO:20.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:21;
- 15 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:21 from nucleotide 170 to nucleotide 2968;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yc14_1 deposited under accession number ATCC 98724;
- 20 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yc14_1 deposited under accession number ATCC 98724;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yc14_1 deposited under accession number ATCC 98724;
- 25 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yc14_1 deposited under accession number ATCC 98724;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:22;
- (h) a polynucleotide encoding a protein comprising a fragment of the
30 amino acid sequence of SEQ ID NO:22 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:22;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

5 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:21.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:21 from nucleotide 170 to nucleotide 2968; the nucleotide sequence of the full-length
10 protein coding sequence of clone yc14_1 deposited under accession number ATCC 98724; or the nucleotide sequence of a mature protein coding sequence of clone yc14_1 deposited under accession number ATCC 98724. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yc14_1 deposited under accession number ATCC 98724. In further preferred
15 embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:22, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having
20 biological activity, the fragment comprising the amino acid sequence from amino acid 461 to amino acid 470 of SEQ ID NO:22.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:21.

Further embodiments of the invention provide isolated polynucleotides produced
25 according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

30 (aa) SEQ ID NO:21, but excluding the poly(A) tail at the 3' end of SEQ ID NO:21; and

(ab) the nucleotide sequence of the cDNA insert of clone yc14_1 deposited under accession number ATCC 98724;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

5 and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (ba) SEQ ID NO:21, but excluding the poly(A) tail at the 3' end of SEQ ID NO:21; and

(bb) the nucleotide sequence of the cDNA insert of clone yc14_1 deposited under accession number ATCC 98724;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

15 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:21, and
20 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:21 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:21, but excluding the poly(A) tail at the 3' end of SEQ ID NO:21. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:21 from nucleotide 170 to nucleotide
25 2968, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:21 from nucleotide 170 to nucleotide 2968, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:21 from nucleotide 170 to nucleotide 2968.

In other embodiments, the present invention provides a composition comprising
30 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:22;

(b) a fragment of the amino acid sequence of SEQ ID NO:22, the fragment comprising eight contiguous amino acids of SEQ ID NO:22; and

(c) the amino acid sequence encoded by the cDNA insert of clone yc14_1 deposited under accession number ATCC 98724; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:22. In further preferred
5 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:22, or a protein comprising a fragment of the amino acid sequence of SEQ
10 ID NO:22 having biological activity, the fragment comprising the amino acid sequence from amino acid 461 to amino acid 470 of SEQ ID NO:22.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:23;
- 15 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:23 from nucleotide 82 to nucleotide 729;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yc24_1 deposited under accession number ATCC 98755;
- 20 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yc24_1 deposited under accession number ATCC 98755;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yc24_1 deposited under accession number ATCC 98755;
- 25 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yc24_1 deposited under accession number ATCC 98755;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:24;
- (h) a polynucleotide encoding a protein comprising a fragment of the
30 amino acid sequence of SEQ ID NO:24 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:24;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

5 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:23.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:23 from nucleotide 82 to nucleotide 729; the nucleotide sequence of the full-length
10 protein coding sequence of clone yc24_1 deposited under accession number ATCC 98755; or the nucleotide sequence of a mature protein coding sequence of clone yc24_1 deposited under accession number ATCC 98755. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yc24_1 deposited under accession number ATCC 98755. In further preferred
15 embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:24, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having
20 biological activity, the fragment comprising the amino acid sequence from amino acid 103 to amino acid 112 of SEQ ID NO:24.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:23.

Further embodiments of the invention provide isolated polynucleotides produced
25 according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

30 (aa) SEQ ID NO:23, but excluding the poly(A) tail at the 3' end of SEQ ID NO:23; and

(ab) the nucleotide sequence of the cDNA insert of clone yc24_1 deposited under accession number ATCC 98755;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

5 and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (ba) SEQ ID NO:23, but excluding the poly(A) tail at the 3' end of SEQ ID NO:23; and

(bb) the nucleotide sequence of the cDNA insert of clone yc24_1 deposited under accession number ATCC 98755;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

15 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:23, and
20 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:23 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:23, but excluding the poly(A) tail at the 3' end of SEQ ID NO:23. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:23 from nucleotide 82 to nucleotide
25 729, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:23 from nucleotide 82 to nucleotide 729, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:23 from nucleotide 82 to nucleotide 729.

In other embodiments, the present invention provides a composition comprising
30 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:24;

(b) a fragment of the amino acid sequence of SEQ ID NO:24, the fragment comprising eight contiguous amino acids of SEQ ID NO:24; and

(c) the amino acid sequence encoded by the cDNA insert of clone yc24_1 deposited under accession number ATCC 98755; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:24. In further preferred
5 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:24, or a protein comprising a fragment of the amino acid sequence of SEQ
10 ID NO:24 having biological activity, the fragment comprising the amino acid sequence from amino acid 103 to amino acid 112 of SEQ ID NO:24.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:25;
- 15 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:25 from nucleotide 7 to nucleotide 951;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:25 from nucleotide 61 to nucleotide 951;
- (d) a polynucleotide comprising the nucleotide sequence of the full-
20 length protein coding sequence of clone yc25_1 deposited under accession number ATCC 98755;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yc25_1 deposited under accession number ATCC 98755;
- (f) a polynucleotide comprising the nucleotide sequence of a mature
25 protein coding sequence of clone yc25_1 deposited under accession number ATCC 98755;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yc25_1 deposited under accession number ATCC 98755;
- (h) a polynucleotide encoding a protein comprising the amino acid
30 sequence of SEQ ID NO:26;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:26;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

5 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:25.

10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:25 from nucleotide 7 to nucleotide 951; the nucleotide sequence of SEQ ID NO:25 from nucleotide 61 to nucleotide 951; the nucleotide sequence of the full-length protein coding sequence of clone yc25_1 deposited under accession number ATCC 98755; or the nucleotide sequence of a mature protein coding sequence of clone yc25_1 deposited under
15 accession number ATCC 98755. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yc25_1 deposited under accession number ATCC 98755. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment
20 preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:26, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment comprising the amino acid sequence from amino acid 152 to amino acid 161 of SEQ ID NO:26.

25 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:25.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

30 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:25, but excluding the poly(A) tail at the 3' end of SEQ ID NO:25; and

- (ab) the nucleotide sequence of the cDNA insert of clone yc25_1 deposited under accession number ATCC 98755;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 5 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 10 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:25, but excluding the poly(A) tail at the 3' end of SEQ ID NO:25; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 15 yc25_1 deposited under accession number ATCC 98755;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- 20 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:25, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:25 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:25, but excluding the poly(A) tail at the 3' end of SEQ ID NO:25. Also preferably the
- 25 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:25 from nucleotide 7 to nucleotide 951, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:25 from nucleotide 7 to nucleotide 951, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:25 from nucleotide
- 30 7 to nucleotide 951. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:25 from nucleotide 61 to nucleotide 951, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:25 from

nucleotide 61 to nucleotide 951, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:25 from nucleotide 61 to nucleotide 951.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:26;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:26, the fragment comprising eight contiguous amino acids of SEQ ID NO:26; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone yc25_1 deposited under accession number ATCC 98755;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:26. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:26, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment comprising the amino acid sequence from amino acid 152 to amino acid 161 of SEQ ID NO:26.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:27;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:27 from nucleotide 157 to nucleotide 1083;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ye2_1 deposited under accession number ATCC 98755;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ye2_1 deposited under accession number ATCC 98755;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ye2_1 deposited under accession number ATCC 98755;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ye2_1 deposited under accession number ATCC 98755;

- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:28;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:28;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:27.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:27 from nucleotide 157 to nucleotide 1083; the nucleotide sequence of the full-length protein coding sequence of clone ye2_1 deposited under accession number ATCC 98755; or the nucleotide sequence of a mature protein coding sequence of clone ye2_1 deposited under accession number ATCC 98755. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ye2_1 deposited under accession number ATCC 98755. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:28, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment comprising the amino acid sequence from amino acid 149 to amino acid 158 of SEQ ID NO:28.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:27.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:27, but excluding the poly(A) tail at the 3' end of SEQ ID NO:27; and

(ab) the nucleotide sequence of the cDNA insert of clone ye2_1 deposited under accession number ATCC 98755;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:27, but excluding the poly(A) tail at the 3' end of SEQ ID NO:27; and

(bb) the nucleotide sequence of the cDNA insert of clone ye2_1 deposited under accession number ATCC 98755;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:27, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:27 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:27, but excluding the poly(A) tail at the 3' end of SEQ ID NO:27. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:27 from nucleotide 157 to nucleotide 1083, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:27 from nucleotide 157 to nucleotide 1083, to a nucleotide

sequence corresponding to the 3' end of said sequence of SEQ ID NO:27 from nucleotide 157 to nucleotide 1083.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group

5 consisting of:

- (a) the amino acid sequence of SEQ ID NO:28;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:28, the fragment comprising eight contiguous amino acids of SEQ ID NO:28; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone
10 ye2_1 deposited under accession number ATCC 98755;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:28. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment preferably
15 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:28, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment comprising the amino acid sequence from amino acid 149 to amino acid 158 of SEQ ID NO:28.

In one embodiment, the present invention provides a composition comprising an
20 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:29;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:29 from nucleotide 39 to nucleotide 473;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ya65_1 deposited under accession number ATCC 98834;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ya65_1 deposited under accession number ATCC 98834;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ya65_1 deposited under accession number ATCC
30 98834;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ya65_1 deposited under accession number ATCC 98834;

- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:30;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:30;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:29.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:29 from nucleotide 39 to nucleotide 473; the nucleotide sequence of the full-length protein coding sequence of clone ya65_1 deposited under accession number ATCC 98834; or the nucleotide sequence of a mature protein coding sequence of clone ya65_1 deposited under accession number ATCC 98834. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ya65_1 deposited under accession number ATCC 98834. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:30, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment comprising the amino acid sequence from amino acid 67 to amino acid 76 of SEQ ID NO:30.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:29.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:

- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- 5 (aa) SEQ ID NO:29, but excluding the poly(A) tail at the 3' end of SEQ ID NO:29; and
- (ab) the nucleotide sequence of the cDNA insert of clone ya65_1 deposited under accession number ATCC 98834;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 10 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 15 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:29, but excluding the poly(A) tail at the 3' end of SEQ ID NO:29; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 20 ya65_1 deposited under accession number ATCC 98834;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- 25 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:29, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:29 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:29, but excluding the poly(A) tail at the 3' end of SEQ ID NO:29. Also preferably the
- 30 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:29 from nucleotide 39 to nucleotide 473, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:29 from nucleotide 39 to nucleotide 473, to a nucleotide

sequence corresponding to the 3' end of said sequence of SEQ ID NO:29 from nucleotide 39 to nucleotide 473.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:30;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:30, the fragment comprising eight contiguous amino acids of SEQ ID NO:30; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone ya65_1 deposited under accession number ATCC 98834;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:30. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:30, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment comprising the amino acid sequence from amino acid 67 to amino acid 76 of SEQ ID NO:30.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:31;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:31 from nucleotide 664 to nucleotide 903;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yb60_1 deposited under accession number ATCC 98834;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yb60_1 deposited under accession number ATCC 98834;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yb60_1 deposited under accession number ATCC 98834;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yb60_1 deposited under accession number ATCC 98834;

- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:32;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:32;
- 5 (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- 10 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:31.
- 15 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:31 from nucleotide 664 to nucleotide 903; the nucleotide sequence of the full-length protein coding sequence of clone yb60_1 deposited under accession number ATCC 98834; or the nucleotide sequence of a mature protein coding sequence of clone yb60_1 deposited under accession number ATCC 98834. In other preferred embodiments, the
- 20 polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yb60_1 deposited under accession number ATCC 98834. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment preferably comprising eight (more preferably twenty, most
- 25 preferably thirty) contiguous amino acids of SEQ ID NO:32, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment comprising the amino acid sequence from amino acid 35 to amino acid 44 of SEQ ID NO:32.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:31.

30

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (aa) SEQ ID NO:31, but excluding the poly(A) tail at the 3' end of SEQ ID NO:31; and

(ab) the nucleotide sequence of the cDNA insert of clone yb60_1 deposited under accession number ATCC 98834;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

10 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

15 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:31, but excluding the poly(A) tail at the 3' end of SEQ ID NO:31; and

20 (bb) the nucleotide sequence of the cDNA insert of clone yb60_1 deposited under accession number ATCC 98834;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

25 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:31, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:31 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:31, but excluding the poly(A) tail at the 3' end of SEQ ID NO:31. Also preferably the
30 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:31 from nucleotide 664 to nucleotide 903, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:31 from nucleotide 664 to nucleotide 903, to a nucleotide

sequence corresponding to the 3' end of said sequence of SEQ ID NO:31 from nucleotide 664 to nucleotide 903.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group

5 consisting of:

- (a) the amino acid sequence of SEQ ID NO:32;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:32, the fragment comprising eight contiguous amino acids of SEQ ID NO:32; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone
10 yb60_1 deposited under accession number ATCC 98834;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:32. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment preferably
15 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:32, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment comprising the amino acid sequence from amino acid 35 to amino acid 44 of SEQ ID NO:32.

In one embodiment, the present invention provides a composition comprising an
20 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:33;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:33 from nucleotide 88 to nucleotide 447;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
25 NO:33 from nucleotide 427 to nucleotide 447;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yb139_1 deposited under accession number ATCC 98834;
- (e) a polynucleotide encoding the full-length protein encoded by the
30 cDNA insert of clone yb139_1 deposited under accession number ATCC 98834;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yb139_1 deposited under accession number ATCC 98834;

- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yb139_1 deposited under accession number ATCC 98834;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:34;
- 5 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:34;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- 10 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any
15 one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:33.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:33 from nucleotide 88 to nucleotide 447; the nucleotide sequence of SEQ ID NO:33 from nucleotide 427 to nucleotide 447; the nucleotide sequence of the full-length protein
20 coding sequence of clone yb139_1 deposited under accession number ATCC 98834; or the nucleotide sequence of a mature protein coding sequence of clone yb139_1 deposited under accession number ATCC 98834. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yb139_1 deposited under accession number ATCC 98834. In further preferred
25 embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:34, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having
30 biological activity, the fragment comprising the amino acid sequence from amino acid 55 to amino acid 64 of SEQ ID NO:34.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:33.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

5 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:33, but excluding the poly(A) tail at the 3' end of SEQ ID NO:33; and

10 (ab) the nucleotide sequence of the cDNA insert of clone yb139_1 deposited under accession number ATCC 98834;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

15 and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

20 (ba) SEQ ID NO:33, but excluding the poly(A) tail at the 3' end of SEQ ID NO:33; and

(bb) the nucleotide sequence of the cDNA insert of clone yb139_1 deposited under accession number ATCC 98834;

25 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

30 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:33, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:33 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:33, but excluding the poly(A) tail at the 3' end of SEQ ID NO:33. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:33 from nucleotide 88 to nucleotide

447, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:33 from nucleotide 88 to nucleotide 447, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:33 from nucleotide 88 to nucleotide 447. Also preferably the polynucleotide isolated according to the above
5 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:33 from nucleotide 427 to nucleotide 447, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:33 from nucleotide 427 to nucleotide 447, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:33 from nucleotide 427 to nucleotide 447.

10 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:34;
- (b) a fragment of the amino acid sequence of SEQ ID NO:34, the
15 fragment comprising eight contiguous amino acids of SEQ ID NO:34; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yb139_1 deposited under accession number ATCC 98834;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:34. In further preferred
20 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:34, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment comprising the amino acid sequence
25 from amino acid 55 to amino acid 64 of SEQ ID NO:34.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:35;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID
30 NO:35 from nucleotide 93 to nucleotide 1481;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yc29_1 deposited under accession number ATCC 98834;

- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yc29_1 deposited under accession number ATCC 98834;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yc29_1 deposited under accession number ATCC 98834;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yc29_1 deposited under accession number ATCC 98834;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:36;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:36;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:35.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:35 from nucleotide 93 to nucleotide 1481; the nucleotide sequence of the full-length protein coding sequence of clone yc29_1 deposited under accession number ATCC 98834; or the nucleotide sequence of a mature protein coding sequence of clone yc29_1 deposited under accession number ATCC 98834. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yc29_1 deposited under accession number ATCC 98834. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:36, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having

biological activity, the fragment comprising the amino acid sequence from amino acid 226 to amino acid 235 of SEQ ID NO:36.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:35.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize
in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group
10 consisting of:

(aa) SEQ ID NO:35, but excluding the poly(A) tail at the
3' end of SEQ ID NO:35; and

(ab) the nucleotide sequence of the cDNA insert of clone
yc29_1 deposited under accession number ATCC 98834;

15 (ii) hybridizing said probe(s) to human genomic DNA in
conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the
probe(s);

and

20 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that
hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from
the group consisting of:

(ba) SEQ ID NO:35, but excluding the poly(A) tail at the
25 3' end of SEQ ID NO:35; and

(bb) the nucleotide sequence of the cDNA insert of clone
yc29_1 deposited under accession number ATCC 98834;

(ii) hybridizing said primer(s) to human genomic DNA in
conditions at least as stringent as 4X SSC at 50 degrees C;

30 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:35, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

ID NO:35 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:35, but excluding the poly(A) tail at the 3' end of SEQ ID NO:35. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:35 from nucleotide 93 to nucleotide 1481, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:35 from nucleotide 93 to nucleotide 1481, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:35 from nucleotide 93 to nucleotide 1481.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:36;
- (b) a fragment of the amino acid sequence of SEQ ID NO:36, the fragment comprising eight contiguous amino acids of SEQ ID NO:36; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yc29_1 deposited under accession number ATCC 98834;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:36. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:36, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment comprising the amino acid sequence from amino acid 226 to amino acid 235 of SEQ ID NO:36.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:37;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:37 from nucleotide 482 to nucleotide 751;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:37 from nucleotide 611 to nucleotide 751;

- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yc40_1 deposited under accession number ATCC 98834;
- 5 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yc40_1 deposited under accession number ATCC 98834;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yc40_1 deposited under accession number ATCC 98834;
- 10 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yc40_1 deposited under accession number ATCC 98834;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:38;
- 15 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:38;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 20 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:37.
- 25 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:37 from nucleotide 482 to nucleotide 751; the nucleotide sequence of SEQ ID NO:37 from nucleotide 611 to nucleotide 751; the nucleotide sequence of the full-length protein coding sequence of clone yc40_1 deposited under accession number ATCC 98834; or the nucleotide sequence of a mature protein coding sequence of clone yc40_1 deposited under accession number ATCC 98834. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yc40_1 deposited under accession number ATCC 98834. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment
- 30

preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:38, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment comprising the amino acid sequence from amino acid 40 to amino acid 49 of SEQ ID NO:38.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:37.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 10 (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - 15 (aa) SEQ ID NO:37, but excluding the poly(A) tail at the 3' end of SEQ ID NO:37; and
 - (ab) the nucleotide sequence of the cDNA insert of clone yc40_1 deposited under accession number ATCC 98834;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - 20 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that
 - 25 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (ba) SEQ ID NO:37, but excluding the poly(A) tail at the 3' end of SEQ ID NO:37; and
 - (bb) the nucleotide sequence of the cDNA insert of clone
 - 30 yc40_1 deposited under accession number ATCC 98834;
 - (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
 - (iii) amplifying human DNA sequences; and
 - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:37, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:37 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:37, but
5 excluding the poly(A) tail at the 3' end of SEQ ID NO:37. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:37 from nucleotide 482 to nucleotide 751, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:37 from nucleotide 482 to nucleotide 751, to a nucleotide
10 sequence corresponding to the 3' end of said sequence of SEQ ID NO:37 from nucleotide 482 to nucleotide 751. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:37 from nucleotide 611 to nucleotide 751, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:37 from
15 nucleotide 611 to nucleotide 751, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:37 from nucleotide 611 to nucleotide 751.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 20 (a) the amino acid sequence of SEQ ID NO:38;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:38, the fragment comprising eight contiguous amino acids of SEQ ID NO:38; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone yc40_1 deposited under accession number ATCC 98834;
- 25 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:38. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
30 of SEQ ID NO:38, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment comprising the amino acid sequence from amino acid 40 to amino acid 49 of SEQ ID NO:38.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:39;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:39 from nucleotide 179 to nucleotide 601;
- 5 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:39 from nucleotide 356 to nucleotide 601;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yd10_1 deposited under accession number ATCC 98834;
- 10 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yd10_1 deposited under accession number ATCC 98834;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yd10_1 deposited under accession number ATCC 98834;
- 15 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yd10_1 deposited under accession number ATCC 98834;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:40;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:40;
- 20 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 25 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least
- 30 25% of the length of SEQ ID NO:39.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:39 from nucleotide 179 to nucleotide 601; the nucleotide sequence of SEQ ID NO:39 from nucleotide 356 to nucleotide 601; the nucleotide sequence of the full-length protein coding sequence of clone yd10_1 deposited under accession number ATCC 98834; or the

nucleotide sequence of a mature protein coding sequence of clone yd10_1 deposited under accession number ATCC 98834. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yd10_1 deposited under accession number ATCC 98834. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:40, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment comprising the amino acid sequence from amino acid 65 to amino acid 74 of SEQ ID NO:40.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:39.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:39, but excluding the poly(A) tail at the 3' end of SEQ ID NO:39; and
 - (ab) the nucleotide sequence of the cDNA insert of clone yd10_1 deposited under accession number ATCC 98834;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (ba) SEQ ID NO:39, but excluding the poly(A) tail at the 3' end of SEQ ID NO:39; and

- (bb) the nucleotide sequence of the cDNA insert of clone yd10_1 deposited under accession number ATCC 98834;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 5 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:39, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:39 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:39, but excluding the poly(A) tail at the 3' end of SEQ ID NO:39. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:39 from nucleotide 179 to nucleotide 601, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:39 from nucleotide 179 to nucleotide 601, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:39 from nucleotide 179 to nucleotide 601. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:39 from nucleotide 356 to nucleotide 601, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:39 from nucleotide 356 to nucleotide 601, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:39 from nucleotide 356 to nucleotide 601.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:40;
- (b) a fragment of the amino acid sequence of SEQ ID NO:40, the fragment comprising eight contiguous amino acids of SEQ ID NO:40; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yd10_1 deposited under accession number ATCC 98834;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:40. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment preferably

comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:40, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment comprising the amino acid sequence from amino acid 65 to amino acid 74 of SEQ ID NO:40.

- 5 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:
- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:41;
 - (b) a polynucleotide comprising the nucleotide sequence of SEQ ID
10 NO:41 from nucleotide 324 to nucleotide 1559;
 - (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:41 from nucleotide 387 to nucleotide 1559;
 - (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yf5_1 deposited under accession number
15 ATCC 98834;
 - (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yf5_1 deposited under accession number ATCC 98834;
 - (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yf5_1 deposited under accession number ATCC
20 98834;
 - (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yf5_1 deposited under accession number ATCC 98834;
 - (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:42;
 - (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:42;
 - (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
 - (k) a polynucleotide which encodes a species homologue of the protein
30 of (h) or (i) above ;
 - (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:41.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:41 from nucleotide 324 to nucleotide 1559; the nucleotide sequence of SEQ ID NO:41 from nucleotide 387 to nucleotide 1559; the nucleotide sequence of the full-length protein coding sequence of clone yf5_1 deposited under accession number ATCC 98834; or the nucleotide sequence of a mature protein coding sequence of clone yf5_1 deposited under accession number ATCC 98834. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yf5_1 deposited under accession number ATCC 98834. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:42, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment comprising the amino acid sequence from amino acid 201 to amino acid 210 of SEQ ID NO:42.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:41.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:41, but excluding the poly(A) tail at the 3' end of SEQ ID NO:41; and
 - (ab) the nucleotide sequence of the cDNA insert of clone yf5_1 deposited under accession number ATCC 98834;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:41, but excluding the poly(A) tail at the 3' end of SEQ ID NO:41; and

(bb) the nucleotide sequence of the cDNA insert of clone yf5_1 deposited under accession number ATCC 98834;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:41, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:41 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:41, but excluding the poly(A) tail at the 3' end of SEQ ID NO:41. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:41 from nucleotide 324 to nucleotide 1559, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:41 from nucleotide 324 to nucleotide 1559, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:41 from nucleotide 324 to nucleotide 1559. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:41 from nucleotide 387 to nucleotide 1559, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:41 from nucleotide 387 to nucleotide 1559, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:41 from nucleotide 387 to nucleotide 1559.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:42;

- (b) a fragment of the amino acid sequence of SEQ ID NO:42, the fragment comprising eight contiguous amino acids of SEQ ID NO:42; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yf5_1 deposited under accession number ATCC 98834;
- 5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:42. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 10 of SEQ ID NO:42, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment comprising the amino acid sequence from amino acid 201 to amino acid 210 of SEQ ID NO:42.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:43;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:43 from nucleotide 257 to nucleotide 649;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
- 20 NO:43 from nucleotide 335 to nucleotide 649;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ya67_1 deposited under accession number ATCC 98864;
- (e) a polynucleotide encoding the full-length protein encoded by the
- 25 cDNA insert of clone ya67_1 deposited under accession number ATCC 98864;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ya67_1 deposited under accession number ATCC 98864;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA
- 30 insert of clone ya67_1 deposited under accession number ATCC 98864;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:44;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:44;

5 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

10 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:43.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:43 from nucleotide 257 to nucleotide 649; the nucleotide sequence of SEQ ID NO:43 from nucleotide 335 to nucleotide 649; the nucleotide sequence of the full-length protein coding sequence of clone ya67_1 deposited under accession number ATCC 98864; or the nucleotide sequence of a mature protein coding sequence of clone ya67_1 deposited under accession number ATCC 98864. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ya67_1 deposited under accession number ATCC 98864. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:44, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment comprising the amino acid sequence from amino acid 60 to amino acid 69 of SEQ ID NO:44.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:43.

30 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- 5 (aa) SEQ ID NO:43, but excluding the poly(A) tail at the 3' end of SEQ ID NO:43; and
- (ab) the nucleotide sequence of the cDNA insert of clone ya67_1 deposited under accession number ATCC 98864;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 10 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 15 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:43, but excluding the poly(A) tail at the 3' end of SEQ ID NO:43; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 20 ya67_1 deposited under accession number ATCC 98864;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- 25 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:43, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:43 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:43, but excluding the poly(A) tail at the 3' end of SEQ ID NO:43. Also preferably the
- 30 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:43 from nucleotide 257 to nucleotide 649, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:43 from nucleotide 257 to nucleotide 649, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:43 from nucleotide

257 to nucleotide 649. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:43 from nucleotide 335 to nucleotide 649, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:43 from
5 nucleotide 335 to nucleotide 649, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:43 from nucleotide 335 to nucleotide 649.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:44;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:44, the fragment comprising eight contiguous amino acids of SEQ ID NO:44; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone ya67_1 deposited under accession number ATCC 98864;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:44. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
20 of SEQ ID NO:44, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment comprising the amino acid sequence from amino acid 60 to amino acid 69 of SEQ ID NO:44.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:45;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:45 from nucleotide 89 to nucleotide 787;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ya70_1 deposited under accession number
30 ATCC 98864;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ya70_1 deposited under accession number ATCC 98864;

- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ya70_1 deposited under accession number ATCC 98864;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ya70_1 deposited under accession number ATCC 98864;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:46;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:46;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:45.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:45 from nucleotide 89 to nucleotide 787; the nucleotide sequence of the full-length protein coding sequence of clone ya70_1 deposited under accession number ATCC 98864; or the nucleotide sequence of a mature protein coding sequence of clone ya70_1 deposited under accession number ATCC 98864. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ya70_1 deposited under accession number ATCC 98864. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:46, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment comprising the amino acid sequence from amino acid 111 to amino acid 120 of SEQ ID NO:46.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:45.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 5 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (aa) SEQ ID NO:45, but excluding the poly(A) tail at the
- 10 3' end of SEQ ID NO:45; and
- (ab) the nucleotide sequence of the cDNA insert of clone ya70_1 deposited under accession number ATCC 98864;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 15 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 20 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:45, but excluding the poly(A) tail at the 3' end of SEQ ID NO:45; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 25 ya70_1 deposited under accession number ATCC 98864;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

- 30 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:45, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:45 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:45, but excluding the poly(A) tail at the 3' end of SEQ ID NO:45. Also preferably the

polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:45 from nucleotide 89 to nucleotide 787, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:45 from nucleotide 89 to nucleotide 787, to a nucleotide
5 sequence corresponding to the 3' end of said sequence of SEQ ID NO:45 from nucleotide 89 to nucleotide 787.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:46;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:46, the fragment comprising eight contiguous amino acids of SEQ ID NO:46; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone ya70_1 deposited under accession number ATCC 98864;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:46. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
20 of SEQ ID NO:46, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment comprising the amino acid sequence from amino acid 111 to amino acid 120 of SEQ ID NO:46.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:47;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:47 from nucleotide 1017 to nucleotide 1265;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
30 NO:47 from nucleotide 1068 to nucleotide 1265;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yb51_1 deposited under accession number ATCC 98864;

- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yb51_1 deposited under accession number ATCC 98864;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yb51_1 deposited under accession number ATCC 98864;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yb51_1 deposited under accession number ATCC 98864;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:48;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:48;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:47.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:47 from nucleotide 1017 to nucleotide 1265; the nucleotide sequence of SEQ ID NO:47 from nucleotide 1068 to nucleotide 1265; the nucleotide sequence of the full-length protein coding sequence of clone yb51_1 deposited under accession number ATCC 98864; or the nucleotide sequence of a mature protein coding sequence of clone yb51_1 deposited under accession number ATCC 98864. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yb51_1 deposited under accession number ATCC 98864. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:48, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having

biological activity, the fragment comprising the amino acid sequence from amino acid 36 to amino acid 45 of SEQ ID NO:48.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:47.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

10 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:47, but excluding the poly(A) tail at the 3' end of SEQ ID NO:47; and

(ab) the nucleotide sequence of the cDNA insert of clone yb51_1 deposited under accession number ATCC 98864;

15 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25 (ba) SEQ ID NO:47, but excluding the poly(A) tail at the 3' end of SEQ ID NO:47; and

(bb) the nucleotide sequence of the cDNA insert of clone yb51_1 deposited under accession number ATCC 98864;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

30 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:47, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

ID NO:47 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:47, but excluding the poly(A) tail at the 3' end of SEQ ID NO:47. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:47 from nucleotide 1017 to nucleotide 1265, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:47 from nucleotide 1017 to nucleotide 1265, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:47 from nucleotide 1017 to nucleotide 1265. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:47 from nucleotide 1068 to nucleotide 1265, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:47 from nucleotide 1068 to nucleotide 1265, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:47 from nucleotide 1068 to nucleotide 1265.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:48;
- (b) a fragment of the amino acid sequence of SEQ ID NO:48, the fragment comprising eight contiguous amino acids of SEQ ID NO:48; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yb51_1 deposited under accession number ATCC 98864;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:48. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:48, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment comprising the amino acid sequence from amino acid 36 to amino acid 45 of SEQ ID NO:48.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:49;

- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:49 from nucleotide 13 to nucleotide 306;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yb101_1 deposited under accession number ATCC 98864;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yb101_1 deposited under accession number ATCC 98864;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yb101_1 deposited under accession number ATCC 98864;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yb101_1 deposited under accession number ATCC 98864;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:50;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:50;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:49.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:49 from nucleotide 13 to nucleotide 306; the nucleotide sequence of the full-length protein coding sequence of clone yb101_1 deposited under accession number ATCC 98864; or the nucleotide sequence of a mature protein coding sequence of clone yb101_1 deposited under accession number ATCC 98864. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yb101_1 deposited under accession number ATCC 98864. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein

comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:50, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having
5 biological activity, the fragment comprising the amino acid sequence from amino acid 44 to amino acid 53 of SEQ ID NO:50.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:49.

Further embodiments of the invention provide isolated polynucleotides produced
10 according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

15 (aa) SEQ ID NO:49, but excluding the poly(A) tail at the 3' end of SEQ ID NO:49; and

(ab) the nucleotide sequence of the cDNA insert of clone yb101_1 deposited under accession number ATCC 98864;

20 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

25 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:49, but excluding the poly(A) tail at the 3' end of SEQ ID NO:49; and

30 (bb) the nucleotide sequence of the cDNA insert of clone yb101_1 deposited under accession number ATCC 98864;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:49, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:49 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:49, but excluding the poly(A) tail at the 3' end of SEQ ID NO:49. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:49 from nucleotide 13 to nucleotide 306, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:49 from nucleotide 13 to nucleotide 306, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:49 from nucleotide 13 to nucleotide 306.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:50;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:50, the fragment comprising eight contiguous amino acids of SEQ ID NO:50; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone yb101_1 deposited under accession number ATCC 98864;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:50. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:50, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment comprising the amino acid sequence from amino acid 44 to amino acid 53 of SEQ ID NO:50.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:51;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:51 from nucleotide 284 to nucleotide 706;

- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yb124_1 deposited under accession number ATCC 98864;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yb124_1 deposited under accession number ATCC 98864;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yb124_1 deposited under accession number ATCC 98864;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yb124_1 deposited under accession number ATCC 98864;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:52;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:52;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:51.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:51 from nucleotide 284 to nucleotide 706; the nucleotide sequence of the full-length protein coding sequence of clone yb124_1 deposited under accession number ATCC 98864; or the nucleotide sequence of a mature protein coding sequence of clone yb124_1 deposited under accession number ATCC 98864. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yb124_1 deposited under accession number ATCC 98864. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52 having biological activity, the fragment preferably comprising eight (more preferably twenty, most

preferably thirty) contiguous amino acids of SEQ ID NO:52, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52 having biological activity, the fragment comprising the amino acid sequence from amino acid 65 to amino acid 74 of SEQ ID NO:52.

5 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:51.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - 10 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:51, but excluding the poly(A) tail at the 3' end of SEQ ID NO:51; and
 - 15 (ab) the nucleotide sequence of the cDNA insert of clone yb124_1 deposited under accession number ATCC 98864;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);
 - 20 and
 - (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from
 - 25 the group consisting of:
 - (ba) SEQ ID NO:51, but excluding the poly(A) tail at the 3' end of SEQ ID NO:51; and
 - (bb) the nucleotide sequence of the cDNA insert of clone yb124_1 deposited under accession number ATCC 98864;
 - 30 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
 - (iii) amplifying human DNA sequences; and
 - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:51, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:51 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:51, but
5 excluding the poly(A) tail at the 3' end of SEQ ID NO:51. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:51 from nucleotide 284 to nucleotide 706, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:51 from nucleotide 284 to nucleotide 706, to a nucleotide
10 sequence corresponding to the 3' end of said sequence of SEQ ID NO:51 from nucleotide 284 to nucleotide 706.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 15 (a) the amino acid sequence of SEQ ID NO:52;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:52, the fragment comprising eight contiguous amino acids of SEQ ID NO:52; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone yb124_1 deposited under accession number ATCC 98864;
- 20 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:52. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
25 of SEQ ID NO:52, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52 having biological activity, the fragment comprising the amino acid sequence from amino acid 65 to amino acid 74 of SEQ ID NO:52.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 30 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:53;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:53 from nucleotide 1106 to nucleotide 1447;

- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:53 from nucleotide 1187 to nucleotide 1447;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yb125_1 deposited under accession number ATCC 98864;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yb125_1 deposited under accession number ATCC 98864;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yb125_1 deposited under accession number ATCC 98864;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yb125_1 deposited under accession number ATCC 98864;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:54;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:54;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:53.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:53 from nucleotide 1106 to nucleotide 1447; the nucleotide sequence of SEQ ID NO:53 from nucleotide 1187 to nucleotide 1447; the nucleotide sequence of the full-length protein coding sequence of clone yb125_1 deposited under accession number ATCC 98864; or the nucleotide sequence of a mature protein coding sequence of clone yb125_1 deposited under accession number ATCC 98864. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yb125_1 deposited under accession number ATCC 98864. In further preferred

embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:54, or a polynucleotide encoding
5 a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment comprising the amino acid sequence from amino acid 52 to amino acid 61 of SEQ ID NO:54.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:53.

10 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group
15 consisting of:

(aa) SEQ ID NO:53, but excluding the poly(A) tail at the 3' end of SEQ ID NO:53; and

(ab) the nucleotide sequence of the cDNA insert of clone yb125_1 deposited under accession number ATCC 98864;

20 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

25 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

30 (ba) SEQ ID NO:53, but excluding the poly(A) tail at the 3' end of SEQ ID NO:53; and

(bb) the nucleotide sequence of the cDNA insert of clone yb125_1 deposited under accession number ATCC 98864;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:53, and
5 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:53 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:53, but excluding the poly(A) tail at the 3' end of SEQ ID NO:53. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:53 from nucleotide
10 1106 to nucleotide 1447, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:53 from nucleotide 1106 to nucleotide 1447, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:53 from nucleotide 1106 to nucleotide 1447. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of
15 SEQ ID NO:53 from nucleotide 1187 to nucleotide 1447, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:53 from nucleotide 1187 to nucleotide 1447, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:53 from nucleotide 1187 to nucleotide 1447.

In other embodiments, the present invention provides a composition comprising
20 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:54;
- (b) a fragment of the amino acid sequence of SEQ ID NO:54, the fragment comprising eight contiguous amino acids of SEQ ID NO:54; and
- 25 (c) the amino acid sequence encoded by the cDNA insert of clone yb125_1 deposited under accession number ATCC 98864;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:54. In further preferred embodiments, the present invention provides a protein comprising a fragment of the
30 amino acid sequence of SEQ ID NO:54 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:54, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment comprising the amino acid sequence from amino acid 52 to amino acid 61 of SEQ ID NO:54.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:55;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:55 from nucleotide 28 to nucleotide 417;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yb179_1 deposited under accession number ATCC 98864;
- 10 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yb179_1 deposited under accession number ATCC 98864;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yb179_1 deposited under accession number ATCC 98864;
- 15 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yb179_1 deposited under accession number ATCC 98864;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:56;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:56;
- 20 (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- 25 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least
- 30 25% of the length of SEQ ID NO:55.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:55 from nucleotide 28 to nucleotide 417; the nucleotide sequence of the full-length protein coding sequence of clone yb179_1 deposited under accession number ATCC 98864; or the nucleotide sequence of a mature protein coding sequence of clone yb179_1

deposited under accession number ATCC 98864. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yb179_1 deposited under accession number ATCC 98864. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:56, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment comprising the amino acid sequence from amino acid 60 to amino acid 69 of SEQ ID NO:56.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:55.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 15 (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - 20 (aa) SEQ ID NO:55, but excluding the poly(A) tail at the 3' end of SEQ ID NO:55; and
 - (ab) the nucleotide sequence of the cDNA insert of clone yb179_1 deposited under accession number ATCC 98864;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - 25 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
 - 30 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (ba) SEQ ID NO:55, but excluding the poly(A) tail at the 3' end of SEQ ID NO:55; and

- (bb) the nucleotide sequence of the cDNA insert of clone yb179_1 deposited under accession number ATCC 98864;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 5 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:55, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:55 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:55, but excluding the poly(A) tail at the 3' end of SEQ ID NO:55. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:55 from nucleotide 28 to nucleotide 417, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:55 from nucleotide 28 to nucleotide 417, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:55 from nucleotide 28 to nucleotide 417.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:56;
- (b) a fragment of the amino acid sequence of SEQ ID NO:56, the fragment comprising eight contiguous amino acids of SEQ ID NO:56; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yb179_1 deposited under accession number ATCC 98864;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:56. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:56, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment comprising the amino acid sequence from amino acid 60 to amino acid 69 of SEQ ID NO:56.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:57;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:57 from nucleotide 56 to nucleotide 1084;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:57 from nucleotide 107 to nucleotide 1084;
- 10 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yc48_1 deposited under accession number ATCC 98864;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yc48_1 deposited under accession number ATCC 98864;
- 15 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yc48_1 deposited under accession number ATCC 98864;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yc48_1 deposited under accession number ATCC 98864;
- 20 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:58;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:58;
- 25 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 30 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:57.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:57 from nucleotide 56 to nucleotide 1084; the nucleotide sequence of SEQ ID NO:57

from nucleotide 107 to nucleotide 1084; the nucleotide sequence of the full-length protein coding sequence of clone yc48_1 deposited under accession number ATCC 98864; or the nucleotide sequence of a mature protein coding sequence of clone yc48_1 deposited under accession number ATCC 98864. In other preferred embodiments, the polynucleotide
5 encodes the full-length or a mature protein encoded by the cDNA insert of clone yc48_1 deposited under accession number ATCC 98864. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous
10 amino acids of SEQ ID NO:58, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment comprising the amino acid sequence from amino acid 166 to amino acid 175 of SEQ ID NO:58.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ
15 ID NO:57.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize
20 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:57, but excluding the poly(A) tail at the 3' end of SEQ ID NO:57; and
 - (ab) the nucleotide sequence of the cDNA insert of clone
25 yc48_1 deposited under accession number ATCC 98864;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);
30 and
- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:57, but excluding the poly(A) tail at the 3' end of SEQ ID NO:57; and

(bb) the nucleotide sequence of the cDNA insert of clone yc48_1 deposited under accession number ATCC 98864;

- 5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a
10 nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:57, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:57 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:57, but excluding the poly(A) tail at the 3' end of SEQ ID NO:57. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence
15 corresponding to the cDNA sequence of SEQ ID NO:57 from nucleotide 56 to nucleotide 1084, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:57 from nucleotide 56 to nucleotide 1084, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:57 from nucleotide 56 to nucleotide 1084. Also preferably the polynucleotide isolated according to the above
20 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:57 from nucleotide 107 to nucleotide 1084, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:57 from nucleotide 107 to nucleotide 1084, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:57 from nucleotide 107 to nucleotide 1084.

25 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:58;
- (b) a fragment of the amino acid sequence of SEQ ID NO:58, the
30 fragment comprising eight contiguous amino acids of SEQ ID NO:58; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yc48_1 deposited under accession number ATCC 98864;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:58. In further preferred

embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:58, or a protein comprising a fragment of the amino acid sequence of SEQ
5 ID NO:58 having biological activity, the fragment comprising the amino acid sequence from amino acid 166 to amino acid 175 of SEQ ID NO:58.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 10 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:59;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:59 from nucleotide 373 to nucleotide 660;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:59 from nucleotide 436 to nucleotide 660;
- 15 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ye21_1 deposited under accession number ATCC 98864;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ye21_1 deposited under accession number ATCC 98864;
- 20 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ye21_1 deposited under accession number ATCC 98864;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ye21_1 deposited under accession number ATCC 98864;
- 25 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:60;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:60;
- 30 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:59.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:59 from nucleotide 373 to nucleotide 660; the nucleotide sequence of SEQ ID NO:59 from nucleotide 436 to nucleotide 660; the nucleotide sequence of the full-length protein coding sequence of clone ye21_1 deposited under accession number ATCC 98864; or the nucleotide sequence of a mature protein coding sequence of clone ye21_1 deposited under accession number ATCC 98864. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ye21_1 deposited under accession number ATCC 98864. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:60, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment comprising the amino acid sequence from amino acid 43 to amino acid 52 of SEQ ID NO:60.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:59.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (aa) SEQ ID NO:59, but excluding the poly(A) tail at the 3' end of SEQ ID NO:59; and
- (ab) the nucleotide sequence of the cDNA insert of clone ye21_1 deposited under accession number ATCC 98864;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

5 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:59, but excluding the poly(A) tail at the 3' end of SEQ ID NO:59; and

10 (bb) the nucleotide sequence of the cDNA insert of clone ye21_1 deposited under accession number ATCC 98864;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

15 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:59, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:59 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:59, but
20 excluding the poly(A) tail at the 3' end of SEQ ID NO:59. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:59 from nucleotide 373 to nucleotide 660, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:59 from nucleotide 373 to nucleotide 660, to a nucleotide
25 sequence corresponding to the 3' end of said sequence of SEQ ID NO:59 from nucleotide 373 to nucleotide 660. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:59 from nucleotide 436 to nucleotide 660, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:59 from
30 nucleotide 436 to nucleotide 660, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:59 from nucleotide 436 to nucleotide 660.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:60;
- (b) a fragment of the amino acid sequence of SEQ ID NO:60, the fragment comprising eight contiguous amino acids of SEQ ID NO:60; and
- (c) the amino acid sequence encoded by the cDNA insert of clone
5 ye21_1 deposited under accession number ATCC 98864;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:60. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment preferably
10 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:60, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment comprising the amino acid sequence from amino acid 43 to amino acid 52 of SEQ ID NO:60.

In one embodiment, the present invention provides a composition comprising an
15 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:61;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:61 from nucleotide 119 to nucleotide 466;
- 20 (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ye22_1 deposited under accession number ATCC 98864;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ye22_1 deposited under accession number ATCC 98864;
- 25 (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ye22_1 deposited under accession number ATCC 98864;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ye22_1 deposited under accession number ATCC 98864;
- 30 (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:62;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:62;

- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
 - (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
 - 5 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
 - (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:61.
- 10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:61 from nucleotide 119 to nucleotide 466; the nucleotide sequence of the full-length protein coding sequence of clone ye22_1 deposited under accession number ATCC 98864; or the nucleotide sequence of a mature protein coding sequence of clone ye22_1 deposited under accession number ATCC 98864. In other preferred embodiments, the
- 15 polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ye22_1 deposited under accession number ATCC 98864. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment preferably comprising eight (more preferably twenty, most
- 20 preferably thirty) contiguous amino acids of SEQ ID NO:62, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment comprising the amino acid sequence from amino acid 53 to amino acid 62 of SEQ ID NO:62.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ
25 ID NO:61.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize
30 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:61, but excluding the poly(A) tail at the 3' end of SEQ ID NO:61; and

- (ab) the nucleotide sequence of the cDNA insert of clone ye22_1 deposited under accession number ATCC 98864;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 5 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 10 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:61, but excluding the poly(A) tail at the 3' end of SEQ ID NO:61; and
- (bb) the nucleotide sequence of the cDNA insert of clone ye22_1 deposited under accession number ATCC 98864;
- 15 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- 20 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:61, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:61 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:61, but excluding the poly(A) tail at the 3' end of SEQ ID NO:61. Also preferably the
- 25 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:61 from nucleotide 119 to nucleotide 466, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:61 from nucleotide 119 to nucleotide 466, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:61 from nucleotide
- 30 119 to nucleotide 466.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:62;

- (b) a fragment of the amino acid sequence of SEQ ID NO:62, the fragment comprising eight contiguous amino acids of SEQ ID NO:62; and
- (c) the amino acid sequence encoded by the cDNA insert of clone ye22_1 deposited under accession number ATCC 98864;
- 5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:62. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 10 of SEQ ID NO:62, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment comprising the amino acid sequence from amino acid 53 to amino acid 62 of SEQ ID NO:62.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:63;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:63 from nucleotide 1212 to nucleotide 1502;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ye39_1 deposited under accession number
- 20 ATCC 98861;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ye39_1 deposited under accession number ATCC 98861;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ye39_1 deposited under accession number ATCC
- 25 98861;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ye39_1 deposited under accession number ATCC 98861;
- (g) a polynucleotide encoding a protein comprising the amino acid
- 30 sequence of SEQ ID NO:64;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:64;

- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
 - (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
 - 5 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
 - (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:63.
- 10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:63 from nucleotide 1212 to nucleotide 1502; the nucleotide sequence of the full-length protein coding sequence of clone ye39_1 deposited under accession number ATCC 98861; or the nucleotide sequence of a mature protein coding sequence of clone ye39_1 deposited under accession number ATCC 98861. In other preferred embodiments, the
- 15 polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ye39_1 deposited under accession number ATCC 98861. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment preferably comprising eight (more preferably twenty, most
- 20 preferably thirty) contiguous amino acids of SEQ ID NO:64, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment comprising the amino acid sequence from amino acid 43 to amino acid 52 of SEQ ID NO:64.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ
25 ID NO:63.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize
30 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:63, but excluding the poly(A) tail at the 3' end of SEQ ID NO:63; and

- (ab) the nucleotide sequence of the cDNA insert of clone ye39_1 deposited under accession number ATCC 98861;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 5 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 10 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:63, but excluding the poly(A) tail at the 3' end of SEQ ID NO:63; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 15 ye39_1 deposited under accession number ATCC 98861;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- 20 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:63, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:63 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:63, but excluding the poly(A) tail at the 3' end of SEQ ID NO:63. Also preferably the
- 25 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:63 from nucleotide 1212 to nucleotide 1502, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:63 from nucleotide 1212 to nucleotide 1502, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:63 from nucleotide
- 30 1212 to nucleotide 1502.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:64;

- (b) a fragment of the amino acid sequence of SEQ ID NO:64, the fragment comprising eight contiguous amino acids of SEQ ID NO:64; and
- (c) the amino acid sequence encoded by the cDNA insert of clone ye39_1 deposited under accession number ATCC 98861;
- 5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:64. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 10 of SEQ ID NO:64, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment comprising the amino acid sequence from amino acid 43 to amino acid 52 of SEQ ID NO:64.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:65;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:65 from nucleotide 81 to nucleotide 887;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yf9_1 deposited under accession number
- 20 ATCC 98861;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yf9_1 deposited under accession number ATCC 98861;
- (e) a polynucleotide comprising the nucleotide sequence of a mature
- 25 protein coding sequence of clone yf9_1 deposited under accession number ATCC 98861;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yf9_1 deposited under accession number ATCC 98861;
- (g) a polynucleotide encoding a protein comprising the amino acid
- 30 sequence of SEQ ID NO:66;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:66;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

5 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:65.

10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:65 from nucleotide 81 to nucleotide 887; the nucleotide sequence of the full-length protein coding sequence of clone yf9_1 deposited under accession number ATCC 98861; or the nucleotide sequence of a mature protein coding sequence of clone yf9_1 deposited under accession number ATCC 98861. In other preferred embodiments, the
15 polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yf9_1 deposited under accession number ATCC 98861. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66 having biological activity, the fragment preferably comprising eight (more preferably twenty, most
20 preferably thirty) contiguous amino acids of SEQ ID NO:66, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66 having biological activity, the fragment comprising the amino acid sequence from amino acid 129 to amino acid 138 of SEQ ID NO:66.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ
25 ID NO:65.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize
30 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:65; and

(ab) the nucleotide sequence of the cDNA insert of clone yf9_1 deposited under accession number ATCC 98861;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

5 and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (ba) SEQ ID NO:65; and

(bb) the nucleotide sequence of the cDNA insert of clone yf9_1 deposited under accession number ATCC 98861;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

15 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:65, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:65 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:65. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:65 from nucleotide 81 to nucleotide 887, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:65 from nucleotide 81 to nucleotide 887, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:65 from nucleotide 81 to nucleotide 887.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

30 (a) the amino acid sequence of SEQ ID NO:66;

(b) a fragment of the amino acid sequence of SEQ ID NO:66, the fragment comprising eight contiguous amino acids of SEQ ID NO:66; and

(c) the amino acid sequence encoded by the cDNA insert of clone yf9_1 deposited under accession number ATCC 98861;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:66. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66 having biological activity, the fragment preferably
5 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:66, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66 having biological activity, the fragment comprising the amino acid sequence from amino acid 129 to amino acid 138 of SEQ ID NO:66.

In one embodiment, the present invention provides a composition comprising an
10 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:67;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:67 from nucleotide 63 to nucleotide 305;
- 15 (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yh4_1 deposited under accession number ATCC 98861;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yh4_1 deposited under accession number ATCC 98861;
- 20 (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yh4_1 deposited under accession number ATCC 98861;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yh4_1 deposited under accession number ATCC 98861;
- 25 (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:68;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:68;
- 30 (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:67.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:67 from nucleotide 63 to nucleotide 305; the nucleotide sequence of the full-length protein coding sequence of clone yh4_1 deposited under accession number ATCC 98861; or the nucleotide sequence of a mature protein coding sequence of clone yh4_1 deposited under accession number ATCC 98861. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yh4_1 deposited under accession number ATCC 98861. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:68, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68 having biological activity, the fragment comprising the amino acid sequence from amino acid 35 to amino acid 44 of SEQ ID NO:68.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:67.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:67, but excluding the poly(A) tail at the 3' end of SEQ ID NO:67; and

(ab) the nucleotide sequence of the cDNA insert of clone yh4_1 deposited under accession number ATCC 98861;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

5 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:67, but excluding the poly(A) tail at the 3' end of SEQ ID NO:67; and

10 (bb) the nucleotide sequence of the cDNA insert of clone yh4_1 deposited under accession number ATCC 98861;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

15 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:67, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:67 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:67, but
20 excluding the poly(A) tail at the 3' end of SEQ ID NO:67. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:67 from nucleotide 63 to nucleotide 305, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:67 from nucleotide 63 to nucleotide 305, to a nucleotide
25 sequence corresponding to the 3' end of said sequence of SEQ ID NO:67 from nucleotide 63 to nucleotide 305.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

30 (a) the amino acid sequence of SEQ ID NO:68;

(b) a fragment of the amino acid sequence of SEQ ID NO:68, the fragment comprising eight contiguous amino acids of SEQ ID NO:68; and

(c) the amino acid sequence encoded by the cDNA insert of clone yh4_1 deposited under accession number ATCC 98861;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:68. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:68, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68 having biological activity, the fragment comprising the amino acid sequence from amino acid 35 to amino acid 44 of SEQ ID NO:68.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:69;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:69 from nucleotide 332 to nucleotide 685;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:69 from nucleotide 422 to nucleotide 685;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yi4_1 deposited under accession number ATCC 98861;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yi4_1 deposited under accession number ATCC 98861;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yi4_1 deposited under accession number ATCC 98861;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yi4_1 deposited under accession number ATCC 98861;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:70;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:70 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:70;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

5 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:69.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:69 from nucleotide 332 to nucleotide 685; the nucleotide sequence of SEQ ID NO:69
10 from nucleotide 422 to nucleotide 685; the nucleotide sequence of the full-length protein coding sequence of clone yi4_1 deposited under accession number ATCC 98861; or the nucleotide sequence of a mature protein coding sequence of clone yi4_1 deposited under accession number ATCC 98861. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yi4_1
15 deposited under accession number ATCC 98861. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:70 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:70, or a polynucleotide encoding a protein comprising a
20 fragment of the amino acid sequence of SEQ ID NO:70 having biological activity, the fragment comprising the amino acid sequence from amino acid 54 to amino acid 63 of SEQ ID NO:70.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:69.

25 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize
30 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:69, but excluding the poly(A) tail at the 3' end of SEQ ID NO:69; and

(ab) the nucleotide sequence of the cDNA insert of clone yi4_1 deposited under accession number ATCC 98861;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

5 and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (ba) SEQ ID NO:69, but excluding the poly(A) tail at the 3' end of SEQ ID NO:69; and

(bb) the nucleotide sequence of the cDNA insert of clone yi4_1 deposited under accession number ATCC 98861;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

15 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:69, and
20 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:69 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:69, but excluding the poly(A) tail at the 3' end of SEQ ID NO:69. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:69 from nucleotide 332 to nucleotide
25 685, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:69 from nucleotide 332 to nucleotide 685, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:69 from nucleotide 332 to nucleotide 685. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID
30 NO:69 from nucleotide 422 to nucleotide 685, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:69 from nucleotide 422 to nucleotide 685, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:69 from nucleotide 422 to nucleotide 685.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:70;
- 5 (b) a fragment of the amino acid sequence of SEQ ID NO:70, the fragment comprising eight contiguous amino acids of SEQ ID NO:70; and
- (c) the amino acid sequence encoded by the cDNA insert of clone y14_1 deposited under accession number ATCC 98861;

the protein being substantially free from other mammalian proteins. Preferably such
10 protein comprises the amino acid sequence of SEQ ID NO:70. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:70 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:70, or a protein comprising a fragment of the amino acid sequence of SEQ
15 ID NO:70 having biological activity, the fragment comprising the amino acid sequence from amino acid 54 to amino acid 63 of SEQ ID NO:70.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID
20 NO:71;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:71 from nucleotide 143 to nucleotide 502;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:71 from nucleotide 203 to nucleotide 502;
- 25 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yj3_1 deposited under accession number ATCC 98861;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yj3_1 deposited under accession number ATCC 98861;
- 30 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yj3_1 deposited under accession number ATCC 98861;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yj3_1 deposited under accession number ATCC 98861;

- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:72;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:72;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:71.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:71 from nucleotide 143 to nucleotide 502; the nucleotide sequence of SEQ ID NO:71 from nucleotide 203 to nucleotide 502; the nucleotide sequence of the full-length protein coding sequence of clone yj3_1 deposited under accession number ATCC 98861; or the nucleotide sequence of a mature protein coding sequence of clone yj3_1 deposited under accession number ATCC 98861. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yj3_1 deposited under accession number ATCC 98861. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:72, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72 having biological activity, the fragment comprising the amino acid sequence from amino acid 55 to amino acid 64 of SEQ ID NO:72.
- Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:71.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:71, but excluding the poly(A) tail at the 3' end of SEQ ID NO:71; and

(ab) the nucleotide sequence of the cDNA insert of clone yj3_1 deposited under accession number ATCC 98861;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:71, but excluding the poly(A) tail at the 3' end of SEQ ID NO:71; and

(bb) the nucleotide sequence of the cDNA insert of clone yj3_1 deposited under accession number ATCC 98861;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:71, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:71 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:71, but excluding the poly(A) tail at the 3' end of SEQ ID NO:71. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:71 from nucleotide 143 to nucleotide 502, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:71 from nucleotide 143 to nucleotide 502, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:71 from nucleotide

143 to nucleotide 502. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:71 from nucleotide 203 to nucleotide 502, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:71 from
5 nucleotide 203 to nucleotide 502, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:71 from nucleotide 203 to nucleotide 502.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:72;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:72, the fragment comprising eight contiguous amino acids of SEQ ID NO:72; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone yj3_1 deposited under accession number ATCC 98861;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:72. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
20 of SEQ ID NO:72, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72 having biological activity, the fragment comprising the amino acid sequence from amino acid 55 to amino acid 64 of SEQ ID NO:72.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:73;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:73 from nucleotide 30 to nucleotide 1004;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
30 NO:73 from nucleotide 129 to nucleotide 1004;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yj7_1 deposited under accession number ATCC 98861;

- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yj7_1 deposited under accession number ATCC 98861;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yj7_1 deposited under accession number ATCC 98861;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yj7_1 deposited under accession number ATCC 98861;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:74;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:74;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:73.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:73 from nucleotide 30 to nucleotide 1004; the nucleotide sequence of SEQ ID NO:73 from nucleotide 129 to nucleotide 1004; the nucleotide sequence of the full-length protein coding sequence of clone yj7_1 deposited under accession number ATCC 98861; or the nucleotide sequence of a mature protein coding sequence of clone yj7_1 deposited under accession number ATCC 98861. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yj7_1 deposited under accession number ATCC 98861. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:74, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74 having biological activity, the

fragment comprising the amino acid sequence from amino acid 157 to amino acid 166 of SEQ ID NO:74.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:73.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

10 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:73, but excluding the poly(A) tail at the 3' end of SEQ ID NO:73; and

(ab) the nucleotide sequence of the cDNA insert of clone yj7_1 deposited under accession number ATCC 98861;

15 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25 (ba) SEQ ID NO:73, but excluding the poly(A) tail at the 3' end of SEQ ID NO:73; and

(bb) the nucleotide sequence of the cDNA insert of clone yj7_1 deposited under accession number ATCC 98861;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

30 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:73, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

ID NO:73 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:73, but excluding the poly(A) tail at the 3' end of SEQ ID NO:73. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:73 from nucleotide 30 to nucleotide 1004, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:73 from nucleotide 30 to nucleotide 1004, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:73 from nucleotide 30 to nucleotide 1004. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:73 from nucleotide 129 to nucleotide 1004, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:73 from nucleotide 129 to nucleotide 1004, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:73 from nucleotide 129 to nucleotide 1004.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:74;
- (b) a fragment of the amino acid sequence of SEQ ID NO:74, the fragment comprising eight contiguous amino acids of SEQ ID NO:74; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yj7_1 deposited under accession number ATCC 98861;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:74. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:74, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74 having biological activity, the fragment comprising the amino acid sequence from amino acid 157 to amino acid 166 of SEQ ID NO:74.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:75;

- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:75 from nucleotide 109 to nucleotide 1047;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yj10_1 deposited under accession number ATCC 98861;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yj10_1 deposited under accession number ATCC 98861;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yj10_1 deposited under accession number ATCC 98861;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yj10_1 deposited under accession number ATCC 98861;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:76;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:76;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:75.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:75 from nucleotide 109 to nucleotide 1047; the nucleotide sequence of the full-length protein coding sequence of clone yj10_1 deposited under accession number ATCC 98861; or the nucleotide sequence of a mature protein coding sequence of clone yj10_1 deposited under accession number ATCC 98861. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yj10_1 deposited under accession number ATCC 98861. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein

comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:76, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having
5 biological activity, the fragment comprising the amino acid sequence from amino acid 151 to amino acid 160 of SEQ ID NO:76.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:75.

Further embodiments of the invention provide isolated polynucleotides produced
10 according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

15 (aa) SEQ ID NO:75, but excluding the poly(A) tail at the 3' end of SEQ ID NO:75; and

(ab) the nucleotide sequence of the cDNA insert of clone yj10_1 deposited under accession number ATCC 98861;

20 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

25 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:75, but excluding the poly(A) tail at the 3' end of SEQ ID NO:75; and

30 (bb) the nucleotide sequence of the cDNA insert of clone yj10_1 deposited under accession number ATCC 98861;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:75, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:75 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:75, but excluding the poly(A) tail at the 3' end of SEQ ID NO:75. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:75 from nucleotide 109 to nucleotide 1047, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:75 from nucleotide 109 to nucleotide 1047, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:75 from nucleotide 109 to nucleotide 1047.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:76;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:76, the fragment comprising eight contiguous amino acids of SEQ ID NO:76; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone yj10_1 deposited under accession number ATCC 98861;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:76. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:76, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment comprising the amino acid sequence from amino acid 151 to amino acid 160 of SEQ ID NO:76.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:77;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:77 from nucleotide 42 to nucleotide 1196;

- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:77 from nucleotide 558 to nucleotide 1196;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yj28_1 deposited under accession number ATCC 98861;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yj28_1 deposited under accession number ATCC 98861;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yj28_1 deposited under accession number ATCC 98861;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yj28_1 deposited under accession number ATCC 98861;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:78;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:78;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:77. .

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:77 from nucleotide 42 to nucleotide 1196; the nucleotide sequence of SEQ ID NO:77 from nucleotide 558 to nucleotide 1196; the nucleotide sequence of the full-length protein coding sequence of clone yj28_1 deposited under accession number ATCC 98861; or the nucleotide sequence of a mature protein coding sequence of clone yj28_1 deposited under accession number ATCC 98861. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yj28_1 deposited under accession number ATCC 98861. In further preferred embodiments, the

present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:78, or a polynucleotide encoding a protein comprising a
5 fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment comprising the amino acid sequence from amino acid 187 to amino acid 196 of SEQ ID NO:78.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:77.

10 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group
15 consisting of:

(aa) SEQ ID NO:77, but excluding the poly(A) tail at the 3' end of SEQ ID NO:77; and

(ab) the nucleotide sequence of the cDNA insert of clone yj28_1 deposited under accession number ATCC 98861;

20 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

25 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

30 (ba) SEQ ID NO:77, but excluding the poly(A) tail at the 3' end of SEQ ID NO:77; and

(bb) the nucleotide sequence of the cDNA insert of clone yj28_1 deposited under accession number ATCC 98861;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:77, and
5 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:77 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:77, but excluding the poly(A) tail at the 3' end of SEQ ID NO:77. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:77 from nucleotide 42 to nucleotide
10 1196, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:77 from nucleotide 42 to nucleotide 1196, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:77 from nucleotide 42 to nucleotide 1196. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID
15 NO:77 from nucleotide 558 to nucleotide 1196, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:77 from nucleotide 558 to nucleotide 1196, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:77 from nucleotide 558 to nucleotide 1196.

In other embodiments, the present invention provides a composition comprising
20 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:78;
- (b) a fragment of the amino acid sequence of SEQ ID NO:78, the fragment comprising eight contiguous amino acids of SEQ ID NO:78; and
- 25 (c) the amino acid sequence encoded by the cDNA insert of clone yj28_1 deposited under accession number ATCC 98861;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:78. In further preferred embodiments, the present invention provides a protein comprising a fragment of the
30 amino acid sequence of SEQ ID NO:78 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:78, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment comprising the amino acid sequence from amino acid 187 to amino acid 196 of SEQ ID NO:78.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:79;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:79 from nucleotide 29 to nucleotide 1156;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:79 from nucleotide 995 to nucleotide 1156;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yj29_1 deposited under accession number ATCC 98861;
- 10 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yj29_1 deposited under accession number ATCC 98861;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yj29_1 deposited under accession number ATCC 98861;
- 15 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yj29_1 deposited under accession number ATCC 98861;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:80;
- 20 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:80;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- 25 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 30 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:79.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:79 from nucleotide 29 to nucleotide 1156; the nucleotide sequence of SEQ ID NO:79

from nucleotide 995 to nucleotide 1156; the nucleotide sequence of the full-length protein coding sequence of clone yj29_1 deposited under accession number ATCC 98861; or the nucleotide sequence of a mature protein coding sequence of clone yj29_1 deposited under accession number ATCC 98861. In other preferred embodiments, the polynucleotide
5 encodes the full-length or a mature protein encoded by the cDNA insert of clone yj29_1 deposited under accession number ATCC 98861. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous
10 amino acids of SEQ ID NO:80, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment comprising the amino acid sequence from amino acid 183 to amino acid 192 of SEQ ID NO:80.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ
15 ID NO:79.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize
20 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:79, but excluding the poly(A) tail at the 3' end of SEQ ID NO:79; and
 - (ab) the nucleotide sequence of the cDNA insert of clone
25 yj29_1 deposited under accession number ATCC 98861;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);
30
- and
- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:79, but excluding the poly(A) tail at the 3' end of SEQ ID NO:79; and

(bb) the nucleotide sequence of the cDNA insert of clone yj29_1 deposited under accession number ATCC 98861;

5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a
10 nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:79, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:79 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:79, but excluding the poly(A) tail at the 3' end of SEQ ID NO:79. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence
15 corresponding to the cDNA sequence of SEQ ID NO:79 from nucleotide 29 to nucleotide 1156, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:79 from nucleotide 29 to nucleotide 1156, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:79 from nucleotide 29 to nucleotide 1156. Also preferably the polynucleotide isolated according to the above
20 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:79 from nucleotide 995 to nucleotide 1156, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:79 from nucleotide 995 to nucleotide 1156, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:79 from nucleotide 995 to nucleotide 1156.

25 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:80;

30 (b) a fragment of the amino acid sequence of SEQ ID NO:80, the fragment comprising eight contiguous amino acids of SEQ ID NO:80; and

(c) the amino acid sequence encoded by the cDNA insert of clone yj29_1 deposited under accession number ATCC 98861;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:80. In further preferred

embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:80, or a protein comprising a fragment of the amino acid sequence of SEQ
5 ID NO:80 having biological activity, the fragment comprising the amino acid sequence from amino acid 183 to amino acid 192 of SEQ ID NO:80.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 10 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:81;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:81 from nucleotide 93 to nucleotide 398;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:81 from nucleotide 321 to nucleotide 398;
- 15 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yj32_1 deposited under accession number ATCC 98861;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yj32_1 deposited under accession number ATCC 98861;
- 20 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yj32_1 deposited under accession number ATCC 98861;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yj32_1 deposited under accession number ATCC 98861;
- 25 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:82;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:82 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:82;
- 30 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:81.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:81 from nucleotide 93 to nucleotide 398; the nucleotide sequence of SEQ ID NO:81 from nucleotide 321 to nucleotide 398; the nucleotide sequence of the full-length protein coding sequence of clone yj32_1 deposited under accession number ATCC 98861; or the nucleotide sequence of a mature protein coding sequence of clone yj32_1 deposited under accession number ATCC 98861. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yj32_1 deposited under accession number ATCC 98861. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:82 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:82, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:82 having biological activity, the fragment comprising the amino acid sequence from amino acid 46 to amino acid 55 of SEQ ID NO:82.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:81.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:81, but excluding the poly(A) tail at the 3' end of SEQ ID NO:81; and
 - (ab) the nucleotide sequence of the cDNA insert of clone yj32_1 deposited under accession number ATCC 98861;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

5 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:81, but excluding the poly(A) tail at the 3' end of SEQ ID NO:81; and

10 (bb) the nucleotide sequence of the cDNA insert of clone yj32_1 deposited under accession number ATCC 98861;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

15 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:81, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:81 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:81, but
20 excluding the poly(A) tail at the 3' end of SEQ ID NO:81. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:81 from nucleotide 93 to nucleotide 398, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:81 from nucleotide 93 to nucleotide 398, to a nucleotide
25 sequence corresponding to the 3' end of said sequence of SEQ ID NO:81 from nucleotide 93 to nucleotide 398. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:81 from nucleotide 321 to nucleotide 398, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:81 from
30 nucleotide 321 to nucleotide 398, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:81 from nucleotide 321 to nucleotide 398.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:82;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:82, the fragment comprising eight contiguous amino acids of SEQ ID NO:82; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone yj32_1 deposited under accession number ATCC 98861;
- 5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:82. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:82 having biological activity, the fragment preferably
- 10 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:82, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:82 having biological activity, the fragment comprising the amino acid sequence from amino acid 46 to amino acid 55 of SEQ ID NO:82.

In one embodiment, the present invention provides a composition comprising an

15 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:83;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:83 from nucleotide 167 to nucleotide 1264;
- 20 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:83 from nucleotide 233 to nucleotide 1264;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yb186_1 deposited under accession number ATCC 98872;
- 25 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yb186_1 deposited under accession number ATCC 98872;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yb186_1 deposited under accession number ATCC 98872;
- 30 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yb186_1 deposited under accession number ATCC 98872;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:84;

- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:84 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:84;
- 5 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 10 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:83.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:83 from nucleotide 167 to nucleotide 1264; the nucleotide sequence of SEQ ID NO:83 from nucleotide 233 to nucleotide 1264; the nucleotide sequence of the full-length protein coding sequence of clone yb186_1 deposited under accession number ATCC 98872; or the nucleotide sequence of a mature protein coding sequence of clone yb186_1 deposited under accession number ATCC 98872. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yb186_1 deposited under accession number ATCC 98872. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:84 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:84, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:84 having biological activity, the fragment comprising the amino acid sequence from amino acid 178 to amino acid 187 of SEQ ID NO:84.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:83.

30 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:

- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- 5 (aa) SEQ ID NO:83, but excluding the poly(A) tail at the 3' end of SEQ ID NO:83; and
- (ab) the nucleotide sequence of the cDNA insert of clone yb186_1 deposited under accession number ATCC 98872;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 10 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 15 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:83, but excluding the poly(A) tail at the 3' end of SEQ ID NO:83; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 20 yb186_1 deposited under accession number ATCC 98872;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- 25 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:83, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:83 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:83, but excluding the poly(A) tail at the 3' end of SEQ ID NO:83. Also preferably the
- 30 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:83 from nucleotide 167 to nucleotide 1264, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:83 from nucleotide 167 to nucleotide 1264, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:83 from nucleotide

167 to nucleotide 1264. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:83 from nucleotide 233 to nucleotide 1264, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:83 from
5 nucleotide 233 to nucleotide 1264, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:83 from nucleotide 233 to nucleotide 1264.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:84;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:84, the fragment comprising eight contiguous amino acids of SEQ ID NO:84; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone yb186_1 deposited under accession number ATCC 98872;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:84. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:84 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
20 of SEQ ID NO:84, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:84 having biological activity, the fragment comprising the amino acid sequence from amino acid 178 to amino acid 187 of SEQ ID NO:84.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:85;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:85 from nucleotide 832 to nucleotide 1416;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yb226_1 deposited under accession
30 number ATCC 98872;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yb226_1 deposited under accession number ATCC 98872;

- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yb226_1 deposited under accession number ATCC 98872;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yb226_1 deposited under accession number ATCC 98872;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:86;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:86 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:86;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:85.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:85 from nucleotide 832 to nucleotide 1416; the nucleotide sequence of the full-length protein coding sequence of clone yb226_1 deposited under accession number ATCC 98872; or the nucleotide sequence of a mature protein coding sequence of clone yb226_1 deposited under accession number ATCC 98872. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yb226_1 deposited under accession number ATCC 98872. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:86 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:86, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:86 having biological activity, the fragment comprising the amino acid sequence from amino acid 92 to amino acid 101 of SEQ ID NO:86.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:85.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 5 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- 10 (aa) SEQ ID NO:85, but excluding the poly(A) tail at the 3' end of SEQ ID NO:85; and
- (ab) the nucleotide sequence of the cDNA insert of clone yb226_1 deposited under accession number ATCC 98872;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 15 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 20 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:85, but excluding the poly(A) tail at the 3' end of SEQ ID NO:85; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 25 yb226_1 deposited under accession number ATCC 98872;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- 30 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:85, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:85 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:85, but excluding the poly(A) tail at the 3' end of SEQ ID NO:85. Also preferably the

polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:85 from nucleotide 832 to nucleotide 1416, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:85 from nucleotide 832 to nucleotide 1416, to a nucleotide
5 sequence corresponding to the 3' end of said sequence of SEQ ID NO:85 from nucleotide 832 to nucleotide 1416.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:86;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:86, the fragment comprising eight contiguous amino acids of SEQ ID NO:86; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone yb226_1 deposited under accession number ATCC 98872;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:86. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:86 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
20 of SEQ ID NO:86, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:86 having biological activity, the fragment comprising the amino acid sequence from amino acid 92 to amino acid 101 of SEQ ID NO:86.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:87;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:87 from nucleotide 155 to nucleotide 745;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yd50_1 deposited under accession
30 number ATCC 98872;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yd50_1 deposited under accession number ATCC 98872;

- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yd50_1 deposited under accession number ATCC 98872;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yd50_1 deposited under accession number ATCC 98872;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:88;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:88;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:87.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:87 from nucleotide 155 to nucleotide 745; the nucleotide sequence of the full-length protein coding sequence of clone yd50_1 deposited under accession number ATCC 98872; or the nucleotide sequence of a mature protein coding sequence of clone yd50_1 deposited under accession number ATCC 98872. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yd50_1 deposited under accession number ATCC 98872. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:88, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment comprising the amino acid sequence from amino acid 93 to amino acid 102 of SEQ ID NO:88.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:87.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 5 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (aa) SEQ ID NO:87, but excluding the poly(A) tail at the
10 3' end of SEQ ID NO:87; and
- (ab) the nucleotide sequence of the cDNA insert of clone yd50_1 deposited under accession number ATCC 98872;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 15 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
20 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:87, but excluding the poly(A) tail at the 3' end of SEQ ID NO:87; and
- (bb) the nucleotide sequence of the cDNA insert of clone
25 yd50_1 deposited under accession number ATCC 98872;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- 30 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:87, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:87 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:87, but excluding the poly(A) tail at the 3' end of SEQ ID NO:87. Also preferably the

polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:87 from nucleotide 155 to nucleotide 745, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:87 from nucleotide 155 to nucleotide 745, to a nucleotide
5 sequence corresponding to the 3' end of said sequence of SEQ ID NO:87 from nucleotide 155 to nucleotide 745.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:88;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:88, the fragment comprising eight contiguous amino acids of SEQ ID NO:88; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone yd50_1 deposited under accession number ATCC 98872;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:88. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
20 of SEQ ID NO:88, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment comprising the amino acid sequence from amino acid 93 to amino acid 102 of SEQ ID NO:88.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:89;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:89 from nucleotide 42 to nucleotide 317;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
30 NO:89 from nucleotide 111 to nucleotide 317;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yd51_1 deposited under accession number ATCC 98872;

- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yd51_1 deposited under accession number ATCC 98872;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yd51_1 deposited under accession number ATCC 98872;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yd51_1 deposited under accession number ATCC 98872;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:90;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:90 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:90;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:89.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:89 from nucleotide 42 to nucleotide 317; the nucleotide sequence of SEQ ID NO:89 from nucleotide 111 to nucleotide 317; the nucleotide sequence of the full-length protein coding sequence of clone yd51_1 deposited under accession number ATCC 98872; or the nucleotide sequence of a mature protein coding sequence of clone yd51_1 deposited under accession number ATCC 98872. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yd51_1 deposited under accession number ATCC 98872. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:90 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:90, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:90 having biological activity, the

fragment comprising the amino acid sequence from amino acid 41 to amino acid 50 of SEQ ID NO:90.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:89.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize
10 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:89, but excluding the poly(A) tail at the
3' end of SEQ ID NO:89; and

(ab) the nucleotide sequence of the cDNA insert of clone
yd51_1 deposited under accession number ATCC 98872;

15 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25 (ba) SEQ ID NO:89, but excluding the poly(A) tail at the 3' end of SEQ ID NO:89; and

(bb) the nucleotide sequence of the cDNA insert of clone yd51_1 deposited under accession number ATCC 98872;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

30 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:89, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

ID NO:89 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:89, but excluding the poly(A) tail at the 3' end of SEQ ID NO:89. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:89 from nucleotide 42 to nucleotide 317, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:89 from nucleotide 42 to nucleotide 317, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:89 from nucleotide 42 to nucleotide 317. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:89 from nucleotide 111 to nucleotide 317, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:89 from nucleotide 111 to nucleotide 317, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:89 from nucleotide 111 to nucleotide 317.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:90;
- (b) a fragment of the amino acid sequence of SEQ ID NO:90, the fragment comprising eight contiguous amino acids of SEQ ID NO:90; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yd51_1 deposited under accession number ATCC 98872;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:90. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:90 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:90, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:90 having biological activity, the fragment comprising the amino acid sequence from amino acid 41 to amino acid 50 of SEQ ID NO:90.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:91;

- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:91 from nucleotide 7 to nucleotide 603;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:91 from nucleotide 244 to nucleotide 603;
- 5 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yd73_1 deposited under accession number ATCC 98872;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yd73_1 deposited under accession number ATCC 98872;
- 10 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yd73_1 deposited under accession number ATCC 98872;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yd73_1 deposited under accession number ATCC 98872;
- 15 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:92;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:92 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:92;
- 20 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 25 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:91.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:91 from nucleotide 7 to nucleotide 603; the nucleotide sequence of SEQ ID NO:91 from nucleotide 244 to nucleotide 603; the nucleotide sequence of the full-length protein coding sequence of clone yd73_1 deposited under accession number ATCC 98872; or the nucleotide sequence of a mature protein coding sequence of clone yd73_1 deposited under accession number ATCC 98872. In other preferred embodiments, the polynucleotide

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encodes the full-length or a mature protein encoded by the cDNA insert of clone yd73_1 deposited under accession number ATCC 98872. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:92 having biological activity, the fragment
5 preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:92, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:92 having biological activity, the fragment comprising the amino acid sequence from amino acid 94 to amino acid 103 of SEQ ID NO:92.

10 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:91.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:
15 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:91, but excluding the poly(A) tail at the
20 3' end of SEQ ID NO:91; and

(ab) the nucleotide sequence of the cDNA insert of clone
yd73_1 deposited under accession number ATCC 98872;

(ii) hybridizing said probe(s) to human genomic DNA in
conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the
25 probe(s);

and

(b) a process comprising the steps of:
(i) preparing one or more polynucleotide primers that
hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from
30 the group consisting of:

(ba) SEQ ID NO:91, but excluding the poly(A) tail at the
3' end of SEQ ID NO:91; and

(bb) the nucleotide sequence of the cDNA insert of clone
yd73_1 deposited under accession number ATCC 98872;

- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
 - (iii) amplifying human DNA sequences; and
 - (iv) isolating the polynucleotide products of step (b)(iii).
- 5 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:91, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:91 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:91, but excluding the poly(A) tail at the 3' end of SEQ ID NO:91. Also preferably the
- 10 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:91 from nucleotide 7 to nucleotide 603, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:91 from nucleotide 7 to nucleotide 603, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:91 from nucleotide
- 15 7 to nucleotide 603. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:91 from nucleotide 244 to nucleotide 603, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:91 from nucleotide 244 to nucleotide 603, to a nucleotide sequence corresponding to the 3' end of
- 20 said sequence of SEQ ID NO:91 from nucleotide 244 to nucleotide 603.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:92;
- 25 (b) a fragment of the amino acid sequence of SEQ ID NO:92, the fragment comprising eight contiguous amino acids of SEQ ID NO:92; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yd73_1 deposited under accession number ATCC 98872;

the protein being substantially free from other mammalian proteins. Preferably such

30 protein comprises the amino acid sequence of SEQ ID NO:92. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:92 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:92, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:92 having biological activity, the fragment comprising the amino acid sequence from amino acid 94 to amino acid 103 of SEQ ID NO:92.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:93;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:93 from nucleotide 367 to nucleotide 747;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
10 NO:93 from nucleotide 667 to nucleotide 747;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ye43_1 deposited under accession number ATCC 98872;
- (e) a polynucleotide encoding the full-length protein encoded by the
15 cDNA insert of clone ye43_1 deposited under accession number ATCC 98872;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ye43_1 deposited under accession number ATCC 98872;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA
20 insert of clone ye43_1 deposited under accession number ATCC 98872;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:94;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment
25 comprising eight contiguous amino acids of SEQ ID NO:94;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:93.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:93 from nucleotide 367 to nucleotide 747; the nucleotide sequence of SEQ ID NO:93 from nucleotide 667 to nucleotide 747; the nucleotide sequence of the full-length protein coding sequence of clone ye43_1 deposited under accession number ATCC 98872; or the

5 nucleotide sequence of a mature protein coding sequence of clone ye43_1 deposited under accession number ATCC 98872. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ye43_1 deposited under accession number ATCC 98872. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment

10 of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:94, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment comprising the amino acid sequence from amino acid 58 to amino acid 67 of SEQ

15 ID NO:94.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:93.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 20 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (aa) SEQ ID NO:93, but excluding the poly(A) tail at the
- 25 3' end of SEQ ID NO:93; and
- (ab) the nucleotide sequence of the cDNA insert of clone ye43_1 deposited under accession number ATCC 98872;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 30 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- 5 (ba) SEQ ID NO:93, but excluding the poly(A) tail at the 3' end of SEQ ID NO:93; and
- (bb) the nucleotide sequence of the cDNA insert of clone ye43_1 deposited under accession number ATCC 98872;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 10 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:93, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:93 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:93, but excluding the poly(A) tail at the 3' end of SEQ ID NO:93. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:93 from nucleotide 367 to nucleotide 747, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:93 from nucleotide 367 to nucleotide 747, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:93 from nucleotide 367 to nucleotide 747. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:93 from nucleotide 667 to nucleotide 747, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:93 from nucleotide 667 to nucleotide 747, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:93 from nucleotide 667 to nucleotide 747.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 30 (a) the amino acid sequence of SEQ ID NO:94;
- (b) a fragment of the amino acid sequence of SEQ ID NO:94, the fragment comprising eight contiguous amino acids of SEQ ID NO:94; and

(c) the amino acid sequence encoded by the cDNA insert of clone ye43_1 deposited under accession number ATCC 98872;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:94. In further preferred
5 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:94, or a protein comprising a fragment of the amino acid sequence of SEQ
10 ID NO:94 having biological activity, the fragment comprising the amino acid sequence from amino acid 58 to amino acid 67 of SEQ ID NO:94.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:95;
- 15 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:95 from nucleotide 632 to nucleotide 1492;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:95 from nucleotide 1460 to nucleotide 1492;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yh71_1 deposited under accession number
20 ATCC 98872;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yh71_1 deposited under accession number ATCC 98872;
- (f) a polynucleotide comprising the nucleotide sequence of a mature
25 protein coding sequence of clone yh71_1 deposited under accession number ATCC 98872;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yh71_1 deposited under accession number ATCC 98872;
- (h) a polynucleotide encoding a protein comprising the amino acid
30 sequence of SEQ ID NO:96;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:96;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

5 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:95.

10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:95 from nucleotide 632 to nucleotide 1492; the nucleotide sequence of SEQ ID NO:95 from nucleotide 1460 to nucleotide 1492; the nucleotide sequence of the full-length protein coding sequence of clone yh71_1 deposited under accession number ATCC 98872; or the nucleotide sequence of a mature protein coding sequence of clone yh71_1 deposited
15 under accession number ATCC 98872. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yh71_1 deposited under accession number ATCC 98872. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological
20 activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:96, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment comprising the amino acid sequence from amino acid 138 to amino acid 147 of SEQ ID NO:96.

25 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:95.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

30 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:95, but excluding the poly(A) tail at the 3' end of SEQ ID NO:95; and

- (ab) the nucleotide sequence of the cDNA insert of clone
yh71_1 deposited under accession number ATCC 98872;
- (ii) hybridizing said probe(s) to human genomic DNA in
conditions at least as stringent as 4X SSC at 50 degrees C; and
- 5 (iii) isolating the DNA polynucleotides detected with the
probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
10 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from
the group consisting of:
- (ba) SEQ ID NO:95, but excluding the poly(A) tail at the
3' end of SEQ ID NO:95; and
- (bb) the nucleotide sequence of the cDNA insert of clone
15 yh71_1 deposited under accession number ATCC 98872;
- (ii) hybridizing said primer(s) to human genomic DNA in
conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- 20 Preferably the polynucleotide isolated according to the above process comprises a
nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:95, and
extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ
ID NO:95 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:95, but
excluding the poly(A) tail at the 3' end of SEQ ID NO:95. Also preferably the
25 polynucleotide isolated according to the above process comprises a nucleotide sequence
corresponding to the cDNA sequence of SEQ ID NO:95 from nucleotide 632 to nucleotide
1492, and extending contiguously from a nucleotide sequence corresponding to the 5' end
of said sequence of SEQ ID NO:95 from nucleotide 632 to nucleotide 1492, to a nucleotide
sequence corresponding to the 3' end of said sequence of SEQ ID NO:95 from nucleotide
30 632 to nucleotide 1492. Also preferably the polynucleotide isolated according to the above
process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID
NO:95 from nucleotide 1460 to nucleotide 1492, and extending contiguously from a
nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:95 from

nucleotide 1460 to nucleotide 1492, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:95 from nucleotide 1460 to nucleotide 1492.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:96;
- (b) a fragment of the amino acid sequence of SEQ ID NO:96, the fragment comprising eight contiguous amino acids of SEQ ID NO:96; and
- (c) the amino acid sequence encoded by the cDNA insert of clone
10 yh71_1 deposited under accession number ATCC 98872;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:96. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment preferably
15 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:96, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment comprising the amino acid sequence from amino acid 138 to amino acid 147 of SEQ ID NO:96.

In one embodiment, the present invention provides a composition comprising an
20 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:97;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:97 from nucleotide 349 to nucleotide 771;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
25 NO:97 from nucleotide 490 to nucleotide 771;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yh100_1 deposited under accession number ATCC 98872;
- (e) a polynucleotide encoding the full-length protein encoded by the
30 cDNA insert of clone yh100_1 deposited under accession number ATCC 98872;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yh100_1 deposited under accession number ATCC 98872;

- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yh100_1 deposited under accession number ATCC 98872;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:98;
- 5 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:98;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- 10 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:97.
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Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:97 from nucleotide 349 to nucleotide 771; the nucleotide sequence of SEQ ID NO:97 from nucleotide 490 to nucleotide 771; the nucleotide sequence of the full-length protein coding sequence of clone yh100_1 deposited under accession number ATCC 98872; or the nucleotide sequence of a mature protein coding sequence of clone yh100_1 deposited under accession number ATCC 98872. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yh100_1 deposited under accession number ATCC 98872. In further preferred

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embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:98, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having

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biological activity, the fragment comprising the amino acid sequence from amino acid 65 to amino acid 74 of SEQ ID NO:98.

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Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:97.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize
5 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:97, but excluding the poly(A) tail at the
3' end of SEQ ID NO:97; and

(ab) the nucleotide sequence of the cDNA insert of clone
10 yh100_1 deposited under accession number ATCC 98872;

(ii) hybridizing said probe(s) to human genomic DNA in
conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the
probe(s);

15 and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that
hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from
the group consisting of:

(ba) SEQ ID NO:97, but excluding the poly(A) tail at the
20 3' end of SEQ ID NO:97; and

(bb) the nucleotide sequence of the cDNA insert of clone
yh100_1 deposited under accession number ATCC 98872;

(ii) hybridizing said primer(s) to human genomic DNA in
25 conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a
nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:97, and
30 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ
ID NO:97 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:97, but
excluding the poly(A) tail at the 3' end of SEQ ID NO:97. Also preferably the
polynucleotide isolated according to the above process comprises a nucleotide sequence
corresponding to the cDNA sequence of SEQ ID NO:97 from nucleotide 349 to nucleotide

771, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:97 from nucleotide 349 to nucleotide 771, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:97 from nucleotide 349 to nucleotide 771. Also preferably the polynucleotide isolated according to the above
5 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:97 from nucleotide 490 to nucleotide 771, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:97 from nucleotide 490 to nucleotide 771, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:97 from nucleotide 490 to nucleotide 771.

10 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:98;
- (b) a fragment of the amino acid sequence of SEQ ID NO:98, the
15 fragment comprising eight contiguous amino acids of SEQ ID NO:98; and
- (c) the amino acid sequence encoded by the cDNA insert of clone
yh100_1 deposited under accession number ATCC 98872;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:98. In further preferred
20 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:98, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment comprising the amino acid sequence
25 from amino acid 65 to amino acid 74 of SEQ ID NO:98.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:99;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID
30 NO:99 from nucleotide 165 to nucleotide 416;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:99 from nucleotide 261 to nucleotide 416;

- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yi3_1 deposited under accession number ATCC 98872;
- 5 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yi3_1 deposited under accession number ATCC 98872;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yi3_1 deposited under accession number ATCC 98872;
- 10 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yi3_1 deposited under accession number ATCC 98872;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:100;
- 15 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:100 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:100;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 20 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:99.
- 25 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:99 from nucleotide 165 to nucleotide 416; the nucleotide sequence of SEQ ID NO:99 from nucleotide 261 to nucleotide 416; the nucleotide sequence of the full-length protein coding sequence of clone yi3_1 deposited under accession number ATCC 98872; or the nucleotide sequence of a mature protein coding sequence of clone yi3_1 deposited under
- 30 accession number ATCC 98872. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yi3_1 deposited under accession number ATCC 98872. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:100 having biological activity, the fragment

preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:100, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:100 having biological activity, the fragment comprising the amino acid sequence from amino acid 37 to amino acid 46 of SEQ ID NO:100.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:99.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 10 (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - 15 (aa) SEQ ID NO:99, but excluding the poly(A) tail at the 3' end of SEQ ID NO:99; and
 - (ab) the nucleotide sequence of the cDNA insert of clone yi3_1 deposited under accession number ATCC 98872;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - 20 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
 - 25 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (ba) SEQ ID NO:99, but excluding the poly(A) tail at the 3' end of SEQ ID NO:99; and
 - 30 (bb) the nucleotide sequence of the cDNA insert of clone yi3_1 deposited under accession number ATCC 98872;
 - (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
 - (iii) amplifying human DNA sequences; and
 - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:99, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:99 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:99, but
5 excluding the poly(A) tail at the 3' end of SEQ ID NO:99. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:99 from nucleotide 165 to nucleotide 416, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:99 from nucleotide 165 to nucleotide 416, to a nucleotide
10 sequence corresponding to the 3' end of said sequence of SEQ ID NO:99 from nucleotide 165 to nucleotide 416. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:99 from nucleotide 261 to nucleotide 416, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:99 from
15 nucleotide 261 to nucleotide 416, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:99 from nucleotide 261 to nucleotide 416.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 20 (a) the amino acid sequence of SEQ ID NO:100;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:100, the fragment comprising eight contiguous amino acids of SEQ ID NO:100; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone yi3_1 deposited under accession number ATCC 98872;
- 25 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:100. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:100 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
30 of SEQ ID NO:100, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:100 having biological activity, the fragment comprising the amino acid sequence from amino acid 37 to amino acid 46 of SEQ ID NO:100.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:101;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:101 from nucleotide 141 to nucleotide 995;
- 5 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:101 from nucleotide 213 to nucleotide 995;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yj23_1 deposited under accession number ATCC 98872;
- 10 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yj23_1 deposited under accession number ATCC 98872;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yj23_1 deposited under accession number ATCC 98872;
- 15 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yj23_1 deposited under accession number ATCC 98872;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:102;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:102;
- 20 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 25 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least
- 30 25% of the length of SEQ ID NO:101.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:101 from nucleotide 141 to nucleotide 995; the nucleotide sequence of SEQ ID NO:101 from nucleotide 213 to nucleotide 995; the nucleotide sequence of the full-length protein coding sequence of clone yj23_1 deposited under accession number ATCC 98872; or the

nucleotide sequence of a mature protein coding sequence of clone yj23_1 deposited under accession number ATCC 98872. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yj23_1 deposited under accession number ATCC 98872. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:102, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment comprising the amino acid sequence from amino acid 137 to amino acid 146 of SEQ ID NO:102.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:101.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:101, but excluding the poly(A) tail at the 3' end of SEQ ID NO:101; and

(ab) the nucleotide sequence of the cDNA insert of clone yj23_1 deposited under accession number ATCC 98872;

(ii) hybridizing said probe(s) to human genomic DNA in

- (bb) the nucleotide sequence of the cDNA insert of clone yj23_1 deposited under accession number ATCC 98872;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 5 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:101, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

10 ID NO:101 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:101, but excluding the poly(A) tail at the 3' end of SEQ ID NO:101. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:101 from nucleotide 141 to nucleotide 995, and extending contiguously from a nucleotide sequence corresponding to the 5' end

15 of said sequence of SEQ ID NO:101 from nucleotide 141 to nucleotide 995, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:101 from nucleotide 141 to nucleotide 995. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:101 from nucleotide 213 to nucleotide 995, and extending contiguously from a

20 nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:101 from

comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:102, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment comprising the amino acid sequence from amino acid 137 to amino acid 146 of SEQ ID NO:102.

5 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:103;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID
10 NO:103 from nucleotide 13 to nucleotide 747;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:103 from nucleotide 67 to nucleotide 747;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone y19_1 deposited under accession number
15 ATCC 98872;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone y19_1 deposited under accession number ATCC 98872;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone y19_1 deposited under accession number ATCC
20 98872;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone y19_1 deposited under accession number ATCC 98872;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:104;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:104;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein
30 of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:103.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:103 from nucleotide 13 to nucleotide 747; the nucleotide sequence of SEQ ID NO:103 from nucleotide 67 to nucleotide 747; the nucleotide sequence of the full-length protein coding sequence of clone yl9_1 deposited under accession number ATCC 98872; or the nucleotide sequence of a mature protein coding sequence of clone yl9_1 deposited under accession number ATCC 98872. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yl9_1 deposited under accession number ATCC 98872. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:104, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment comprising the amino acid sequence from amino acid 117 to amino acid 126 of SEQ ID NO:104.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:103.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:103, but excluding the poly(A) tail at the 3' end of SEQ ID NO:103; and

(ab) the nucleotide sequence of the cDNA insert of clone

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:103, but excluding the poly(A) tail at the 3' end of SEQ ID NO:103; and

(bb) the nucleotide sequence of the cDNA insert of clone y19_1 deposited under accession number ATCC 98872;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:103, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:103 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:103, but excluding the poly(A) tail at the 3' end of SEQ ID NO:103. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:103 from nucleotide 13 to nucleotide 747, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:103 from nucleotide 13 to nucleotide 747, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:103 from nucleotide 13 to nucleotide 747. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:103 from nucleotide 67 to nucleotide 747, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:103 from nucleotide 67 to nucleotide 747, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:103 from nucleotide 67 to nucleotide 747.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:104;

- (b) a fragment of the amino acid sequence of SEQ ID NO:104, the fragment comprising eight contiguous amino acids of SEQ ID NO:104; and
- (c) the amino acid sequence encoded by the cDNA insert of clone y19_1 deposited under accession number ATCC 98872;
- 5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:104. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 10 of SEQ ID NO:104, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment comprising the amino acid sequence from amino acid 117 to amino acid 126 of SEQ ID NO:104.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:105;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:105 from nucleotide 375 to nucleotide 728;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ya66_1 deposited under accession number
- 20 ATCC 98887;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ya66_1 deposited under accession number ATCC 98887;
- (e) a polynucleotide comprising the nucleotide sequence of a mature
- 25 protein coding sequence of clone ya66_1 deposited under accession number ATCC 98887;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ya66_1 deposited under accession number ATCC 98887;
- (g) a polynucleotide encoding a protein comprising the amino acid
- 30 sequence of SEQ ID NO:106;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:106;

- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
 - (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
 - 5 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
 - (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:105.
- 10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:105 from nucleotide 375 to nucleotide 728; the nucleotide sequence of the full-length protein coding sequence of clone ya66_1 deposited under accession number ATCC 98887; or the nucleotide sequence of a mature protein coding sequence of clone ya66_1 deposited under accession number ATCC 98887. In other preferred embodiments, the
- 15 polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ya66_1 deposited under accession number ATCC 98887. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment preferably comprising eight (more preferably twenty, most
- 20 preferably thirty) contiguous amino acids of SEQ ID NO:106, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment comprising the amino acid sequence from amino acid 54 to amino acid 63 of SEQ ID NO:106.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ
25 ID NO:105.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize
30 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:105, but excluding the poly(A) tail at the 3' end of SEQ ID NO:105; and

- (ab) the nucleotide sequence of the cDNA insert of clone ya66_1 deposited under accession number ATCC 98887;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 5 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 10 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:105, but excluding the poly(A) tail at the 3' end of SEQ ID NO:105; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 15 ya66_1 deposited under accession number ATCC 98887;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- 20 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:105, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:105 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:105, but excluding the poly(A) tail at the 3' end of SEQ ID NO:105. Also preferably the
- 25 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:105 from nucleotide 375 to nucleotide 728, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:105 from nucleotide 375 to nucleotide 728, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:105 from nucleotide
- 30 375 to nucleotide 728.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:106;

- (b) a fragment of the amino acid sequence of SEQ ID NO:106, the fragment comprising eight contiguous amino acids of SEQ ID NO:106; and
- (c) the amino acid sequence encoded by the cDNA insert of clone ya66_1 deposited under accession number ATCC 98887;
- 5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:106. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 10 of SEQ ID NO:106, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment comprising the amino acid sequence from amino acid 54 to amino acid 63 of SEQ ID NO:106.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:107;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:107 from nucleotide 131 to nucleotide 457;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yb187_1 deposited under accession
- 20 number ATCC 98887;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yb187_1 deposited under accession number ATCC 98887;
- (e) a polynucleotide comprising the nucleotide sequence of a mature
- 25 protein coding sequence of clone yb187_1 deposited under accession number ATCC 98887;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yb187_1 deposited under accession number ATCC 98887;
- (g) a polynucleotide encoding a protein comprising the amino acid
- 30 sequence of SEQ ID NO:108;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:108 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:108;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

5 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:107.

10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:107 from nucleotide 131 to nucleotide 457; the nucleotide sequence of the full-length protein coding sequence of clone yb187_1 deposited under accession number ATCC 98887; or the nucleotide sequence of a mature protein coding sequence of clone yb187_1 deposited under accession number ATCC 98887. In other preferred embodiments, the
15 polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yb187_1 deposited under accession number ATCC 98887. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:108 having biological activity, the fragment preferably comprising eight (more preferably twenty, most
20 preferably thirty) contiguous amino acids of SEQ ID NO:108, or a polynucleotide

- (ab) the nucleotide sequence of the cDNA insert of clone yb187_1 deposited under accession number ATCC 98887;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 5 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 10 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:107, but excluding the poly(A) tail at the 3' end of SEQ ID NO:107; and
- (bb) the nucleotide sequence of the cDNA insert of clone yb187_1 deposited under accession number ATCC 98887;
- 15 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- 20 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:107, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:107 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:107, but excluding the poly(A) tail at the 3' end of SEQ ID NO:107. Also preferably the
- 25 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:107 from nucleotide 131 to nucleotide 457, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:107 from nucleotide 131 to nucleotide 457, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:107 from nucleotide
- 30 131 to nucleotide 457.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:108;

- (b) a fragment of the amino acid sequence of SEQ ID NO:108, the fragment comprising eight contiguous amino acids of SEQ ID NO:108; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yb187_1 deposited under accession number ATCC 98887;
- 5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:108. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:108 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 10 of SEQ ID NO:108, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:108 having biological activity, the fragment comprising the amino acid sequence from amino acid 49 to amino acid 58 of SEQ ID NO:108.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:109;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:109 from nucleotide 458 to nucleotide 676;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
- 20 NO:109 from nucleotide 503 to nucleotide 676;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yb219_1 deposited under accession number ATCC 98887;
- (e) a polynucleotide encoding the full-length protein encoded by the
- 25 cDNA insert of clone yb219_1 deposited under accession number ATCC 98887;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yb219_1 deposited under accession number ATCC 98887;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA
- 30 insert of clone yb219_1 deposited under accession number ATCC 98887;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:110;

- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:110 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:110;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:109.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:109 from nucleotide 458 to nucleotide 676; the nucleotide sequence of SEQ ID NO:109 from nucleotide 503 to nucleotide 676; the nucleotide sequence of the full-length protein coding sequence of clone yb219_1 deposited under accession number ATCC 98887; or the nucleotide sequence of a mature protein coding sequence of clone yb219_1 deposited under accession number ATCC 98887. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yb219_1 deposited under accession number ATCC 98887. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:110 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:110, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:110 having biological activity, the fragment comprising the amino acid sequence from amino acid 31 to amino acid 40 of SEQ ID NO:110.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:109.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:109, but excluding the poly(A) tail at the 3' end of SEQ ID NO:109; and

(ab) the nucleotide sequence of the cDNA insert of clone yb219_1 deposited under accession number ATCC 98887;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:109, but excluding the poly(A) tail at the 3' end of SEQ ID NO:109; and

(bb) the nucleotide sequence of the cDNA insert of clone yb219_1 deposited under accession number ATCC 98887;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:109, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:109 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:109, but excluding the poly(A) tail at the 3' end of SEQ ID NO:109. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:109 from nucleotide 458 to nucleotide 676, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:109 from nucleotide 458 to nucleotide 676, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:109 from nucleotide

458 to nucleotide 676. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:109 from nucleotide 503 to nucleotide 676, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:109 from
5 nucleotide 503 to nucleotide 676, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:109 from nucleotide 503 to nucleotide 676.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:110;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:110, the fragment comprising eight contiguous amino acids of SEQ ID NO:110; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone yb219_1 deposited under accession number ATCC 98887;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:110. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:110 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
20 of SEQ ID NO:110, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:110 having biological activity, the fragment comprising the amino acid sequence from amino acid 31 to amino acid 40 of SEQ ID NO:110.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:111;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:111 from nucleotide 238 to nucleotide 396;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
30 NO:111 from nucleotide 277 to nucleotide 396;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yb228_1 deposited under accession number ATCC 98887;

- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yb228_1 deposited under accession number ATCC 98887;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yb228_1 deposited under accession number ATCC 98887;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yb228_1 deposited under accession number ATCC 98887;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:112;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:112;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:111.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:111 from nucleotide 238 to nucleotide 396; the nucleotide sequence of SEQ ID NO:111 from nucleotide 277 to nucleotide 396; the nucleotide sequence of the full-length protein coding sequence of clone yb228_1 deposited under accession number ATCC 98887; or the nucleotide sequence of a mature protein coding sequence of clone yb228_1 deposited under accession number ATCC 98887. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yb228_1 deposited under accession number ATCC 98887. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:112, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112

having biological activity, the fragment comprising the amino acid sequence from amino acid 21 to amino acid 30 of SEQ ID NO:112.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:111.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

10 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:111, but excluding the poly(A) tail at the 3' end of SEQ ID NO:111; and

(ab) the nucleotide sequence of the cDNA insert of clone yb228_1 deposited under accession number ATCC 98887;

15 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25 (ba) SEQ ID NO:111, but excluding the poly(A) tail at the 3' end of SEQ ID NO:111; and

(bb) the nucleotide sequence of the cDNA insert of clone yb228_1 deposited under accession number ATCC 98887;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

30 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:111, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

ID NO:111 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:111, but excluding the poly(A) tail at the 3' end of SEQ ID NO:111. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:111 from nucleotide 238 to nucleotide 396, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:111 from nucleotide 238 to nucleotide 396, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:111 from nucleotide 238 to nucleotide 396. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:111 from nucleotide 277 to nucleotide 396, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:111 from nucleotide 277 to nucleotide 396, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:111 from nucleotide 277 to nucleotide 396.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:112;
- (b) a fragment of the amino acid sequence of SEQ ID NO:112, the fragment comprising eight contiguous amino acids of SEQ ID NO:112; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yb228_1 deposited under accession number ATCC 98887;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:112. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:112, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment comprising the amino acid sequence from amino acid 21 to amino acid 30 of SEQ ID NO:112.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:113;

- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:113 from nucleotide 6 to nucleotide 722;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:113 from nucleotide 375 to nucleotide 722;
- 5 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yc27_1 deposited under accession number ATCC 98887;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yc27_1 deposited under accession number ATCC 98887;
- 10 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yc27_1 deposited under accession number ATCC 98887;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yc27_1 deposited under accession number ATCC 98887;
- 15 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:114;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:114 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:114;
- 20 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 25 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:113.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:113 from nucleotide 6 to nucleotide 722; the nucleotide sequence of SEQ ID NO:113 from nucleotide 375 to nucleotide 722; the nucleotide sequence of the full-length protein coding sequence of clone yc27_1 deposited under accession number ATCC 98887; or the nucleotide sequence of a mature protein coding sequence of clone yc27_1 deposited under accession number ATCC 98887. In other preferred embodiments, the polynucleotide

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encodes the full-length or a mature protein encoded by the cDNA insert of clone yc27_1 deposited under accession number ATCC 98887. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:114 having biological activity, the fragment
5 preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:114, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:114 having biological activity, the fragment comprising the amino acid sequence from amino acid 114 to amino acid 123 of SEQ ID NO:114.

10 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:113.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - 15 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:113, but excluding the poly(A) tail at the 3' end of SEQ ID NO:113; and
 - 20 (ab) the nucleotide sequence of the cDNA insert of clone yc27_1 deposited under accession number ATCC 98887;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the
25 probe(s);
- and
- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from
30 the group consisting of:
 - (ba) SEQ ID NO:113, but excluding the poly(A) tail at the 3' end of SEQ ID NO:113; and
 - (bb) the nucleotide sequence of the cDNA insert of clone yc27_1 deposited under accession number ATCC 98887;

- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
 - (iii) amplifying human DNA sequences; and
 - (iv) isolating the polynucleotide products of step (b)(iii).
- 5 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:113, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:113 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:113, but excluding the poly(A) tail at the 3' end of SEQ ID NO:113. Also preferably the
- 10 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:113 from nucleotide 6 to nucleotide 722, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:113 from nucleotide 6 to nucleotide 722, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:113 from nucleotide
- 15 6 to nucleotide 722. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:113 from nucleotide 375 to nucleotide 722, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:113 from nucleotide 375 to nucleotide 722, to a nucleotide sequence corresponding to the 3' end of
- 20 said sequence of SEQ ID NO:113 from nucleotide 375 to nucleotide 722.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:114;
- 25 (b) a fragment of the amino acid sequence of SEQ ID NO:114, the fragment comprising eight contiguous amino acids of SEQ ID NO:114; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yc27_1 deposited under accession number ATCC 98887;

the protein being substantially free from other mammalian proteins. Preferably such

30 protein comprises the amino acid sequence of SEQ ID NO:114. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:114 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:114, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:114 having biological activity, the fragment comprising the amino acid sequence from amino acid 114 to amino acid 123 of SEQ ID NO:114.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:115;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:115 from nucleotide 382 to nucleotide 681;
- (c) a polynucleotide comprising the nucleotide sequence of the full-
10 length protein coding sequence of clone yc49_1 deposited under accession number ATCC 98887;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yc49_1 deposited under accession number ATCC 98887;
- (e) a polynucleotide comprising the nucleotide sequence of a mature
15 protein coding sequence of clone yc49_1 deposited under accession number ATCC 98887;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yc49_1 deposited under accession number ATCC 98887;
- (g) a polynucleotide encoding a protein comprising the amino acid
20 sequence of SEQ ID NO:116;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:116 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:116;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of
25 (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:115.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:115 from nucleotide 382 to nucleotide 681; the nucleotide sequence of the full-length

protein coding sequence of clone yc49_1 deposited under accession number ATCC 98887; or the nucleotide sequence of a mature protein coding sequence of clone yc49_1 deposited under accession number ATCC 98887. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yc49_1 deposited under accession number ATCC 98887. In further preferred
5 embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:116 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:116, or a polynucleotide
10 encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:116 having biological activity, the fragment comprising the amino acid sequence from amino acid 45 to amino acid 54 of SEQ ID NO:116.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:115.

15 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group
20 consisting of:
 - (aa) SEQ ID NO:115, but excluding the poly(A) tail at the 3' end of SEQ ID NO:115; and
 - (ab) the nucleotide sequence of the cDNA insert of clone yc49_1 deposited under accession number ATCC 98887;
 - 25 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- 30 (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- (ba) SEQ ID NO:115, but excluding the poly(A) tail at the 3' end of SEQ ID NO:115; and
- (bb) the nucleotide sequence of the cDNA insert of clone yc49_1 deposited under accession number ATCC 98887;
- 5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:115, and
10 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:115 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:115, but excluding the poly(A) tail at the 3' end of SEQ ID NO:115. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence
15 corresponding to the cDNA sequence of SEQ ID NO:115 from nucleotide 382 to nucleotide 681, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:115 from nucleotide 382 to nucleotide 681, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:115 from nucleotide 382 to nucleotide 681.

20 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:116;
- (b) a fragment of the amino acid sequence of SEQ ID NO:116, the
25 fragment comprising eight contiguous amino acids of SEQ ID NO:116; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yc49_1 deposited under accession number ATCC 98887;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:116. In further preferred
30 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:116 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:116, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:116 having biological activity, the fragment comprising the amino acid sequence from amino acid 45 to amino acid 54 of SEQ ID NO:116.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:117;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:117 from nucleotide 71 to nucleotide 364;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yd40_1 deposited under accession
10 number ATCC 98887;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yd40_1 deposited under accession number ATCC 98887;
- (e) a polynucleotide comprising the nucleotide sequence of a mature
15 protein coding sequence of clone yd40_1 deposited under accession number ATCC 98887;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yd40_1 deposited under accession number ATCC 98887;
- (g) a polynucleotide encoding a protein comprising the amino acid
20 sequence of SEQ ID NO:118;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:118 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:118;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of
25 (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:117.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:117 from nucleotide 71 to nucleotide 364; the nucleotide sequence of the full-length

protein coding sequence of clone yd40_1 deposited under accession number ATCC 98887; or the nucleotide sequence of a mature protein coding sequence of clone yd40_1 deposited under accession number ATCC 98887. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yd40_1 deposited under accession number ATCC 98887. In further preferred
5 embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:118 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:118, or a polynucleotide
10 encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:118 having biological activity, the fragment comprising the amino acid sequence from amino acid 44 to amino acid 53 of SEQ ID NO:118.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:117.

15 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group
20 consisting of:

(aa) SEQ ID NO:117, but excluding the poly(A) tail at the 3' end of SEQ ID NO:117; and

(ab) the nucleotide sequence of the cDNA insert of clone yd40_1 deposited under accession number ATCC 98887;

25 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

30 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:117, but excluding the poly(A) tail at the 3' end of SEQ ID NO:117; and

(bb) the nucleotide sequence of the cDNA insert of clone yd40_1 deposited under accession number ATCC 98887;

5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

10 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:117, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:117 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:117, but excluding the poly(A) tail at the 3' end of SEQ ID NO:117. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence
15 corresponding to the cDNA sequence of SEQ ID NO:117 from nucleotide 71 to nucleotide 364, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:117 from nucleotide 71 to nucleotide 364, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:117 from nucleotide 71 to nucleotide 364.

20 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:118;

(b) a fragment of the amino acid sequence of SEQ ID NO:118, the
25 fragment comprising eight contiguous amino acids of SEQ ID NO:118; and

(c) the amino acid sequence encoded by the cDNA insert of clone yd40_1 deposited under accession number ATCC 98887;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:118. In further preferred
30 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:118 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:118, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:118 having biological activity, the fragment comprising the amino acid sequence from amino acid 44 to amino acid 53 of SEQ ID NO:118.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:119;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:119 from nucleotide 75 to nucleotide 725;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yd64_1 deposited under accession
10 number ATCC 98887;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yd64_1 deposited under accession number ATCC 98887;
- (e) a polynucleotide comprising the nucleotide sequence of a mature
15 protein coding sequence of clone yd64_1 deposited under accession number ATCC 98887;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yd64_1 deposited under accession number ATCC 98887;
- (g) a polynucleotide encoding a protein comprising the amino acid
20 sequence of SEQ ID NO:120;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:120 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:120;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of
25 (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:119.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:119 from nucleotide 75 to nucleotide 725; the nucleotide sequence of the full-length

protein coding sequence of clone yd64_1 deposited under accession number ATCC 98887; or the nucleotide sequence of a mature protein coding sequence of clone yd64_1 deposited under accession number ATCC 98887. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yd64_1 deposited under accession number ATCC 98887. In further preferred
5 embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:120 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:120, or a polynucleotide
10 encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:120 having biological activity, the fragment comprising the amino acid sequence from amino acid 103 to amino acid 112 of SEQ ID NO:120.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:119.

15 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize
20 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- (aa) SEQ ID NO:119, but excluding the poly(A) tail at the
3' end of SEQ ID NO:119; and

- (ab) the nucleotide sequence of the cDNA insert of clone
yd64_1 deposited under accession number ATCC 98887;

25 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

- (iii) isolating the DNA polynucleotides detected with the
probe(s);

and

30 (b) a process comprising the steps of:

- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:119, but excluding the poly(A) tail at the 3' end of SEQ ID NO:119; and

(bb) the nucleotide sequence of the cDNA insert of clone yd64_1 deposited under accession number ATCC 98887;

5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

10 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:119, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:119 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:119, but excluding the poly(A) tail at the 3' end of SEQ ID NO:119. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence
15 corresponding to the cDNA sequence of SEQ ID NO:119 from nucleotide 75 to nucleotide 725, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:119 from nucleotide 75 to nucleotide 725, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:119 from nucleotide 75 to nucleotide 725.

20 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:120;

(b) a fragment of the amino acid sequence of SEQ ID NO:120, the
25 fragment comprising eight contiguous amino acids of SEQ ID NO:120; and

(c) the amino acid sequence encoded by the cDNA insert of clone yd64_1 deposited under accession number ATCC 98887;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:120. In further preferred
30 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:120 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:120, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:120 having biological activity, the fragment comprising the amino acid sequence from amino acid 103 to amino acid 112 of SEQ ID NO:120.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:121;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:121 from nucleotide 256 to nucleotide 780;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
10 NO:121 from nucleotide 412 to nucleotide 780;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ye47_1 deposited under accession number ATCC 98887;
- (e) a polynucleotide encoding the full-length protein encoded by the
15 cDNA insert of clone ye47_1 deposited under accession number ATCC 98887;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ye47_1 deposited under accession number ATCC 98887;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA
20 insert of clone ye47_1 deposited under accession number ATCC 98887;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:122;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:122 having biological activity, the fragment
25 comprising eight contiguous amino acids of SEQ ID NO:122;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:121.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:121 from nucleotide 256 to nucleotide 780; the nucleotide sequence of SEQ ID NO:121 from nucleotide 412 to nucleotide 780; the nucleotide sequence of the full-length protein coding sequence of clone ye47_1 deposited under accession number ATCC 98887; or the
5 nucleotide sequence of a mature protein coding sequence of clone ye47_1 deposited under accession number ATCC 98887. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ye47_1 deposited under accession number ATCC 98887. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment
10 of the amino acid sequence of SEQ ID NO:122 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:122, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:122 having biological activity, the fragment comprising the amino acid sequence from amino acid 82 to amino acid 91 of SEQ
15 ID NO:122.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:121.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 20 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:121, but excluding the poly(A) tail at the
25 3' end of SEQ ID NO:121; and
 - (ab) the nucleotide sequence of the cDNA insert of clone ye47_1 deposited under accession number ATCC 98887;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - 30 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (ba) SEQ ID NO:121, but excluding the poly(A) tail at the 3' end of SEQ ID NO:121; and

(bb) the nucleotide sequence of the cDNA insert of clone ye47_1 deposited under accession number ATCC 98887;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

10 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:121, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ
15 ID NO:121 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:121, but excluding the poly(A) tail at the 3' end of SEQ ID NO:121. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:121 from nucleotide 256 to nucleotide 780, and extending contiguously from a nucleotide sequence corresponding to the 5' end
20 of said sequence of SEQ ID NO:121 from nucleotide 256 to nucleotide 780, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:121 from nucleotide 256 to nucleotide 780. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:121 from nucleotide 412 to nucleotide 780, and extending contiguously from a
25 nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:121 from nucleotide 412 to nucleotide 780, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:121 from nucleotide 412 to nucleotide 780.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group
30 consisting of:

(a) the amino acid sequence of SEQ ID NO:122;

(b) a fragment of the amino acid sequence of SEQ ID NO:122, the fragment comprising eight contiguous amino acids of SEQ ID NO:122; and

(c) the amino acid sequence encoded by the cDNA insert of clone ye47_1 deposited under accession number ATCC 98887; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:122. In further preferred
5 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:122 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:122, or a protein comprising a fragment of the amino acid sequence of SEQ
10 ID NO:122 having biological activity, the fragment comprising the amino acid sequence from amino acid 82 to amino acid 91 of SEQ ID NO:122.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:123;
- 15 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:123 from nucleotide 127 to nucleotide 405;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:123 from nucleotide 268 to nucleotide 405;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yh50_1 deposited under accession number
20 ATCC 98887;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yh50_1 deposited under accession number ATCC 98887;
- (f) a polynucleotide comprising the nucleotide sequence of a mature
25 protein coding sequence of clone yh50_1 deposited under accession number ATCC 98887;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yh50_1 deposited under accession number ATCC 98887;
- (h) a polynucleotide encoding a protein comprising the amino acid
30 sequence of SEQ ID NO:124;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:124 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:124;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

5 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:123.

10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:123 from nucleotide 127 to nucleotide 405; the nucleotide sequence of SEQ ID NO:123 from nucleotide 268 to nucleotide 405; the nucleotide sequence of the full-length protein coding sequence of clone yh50_1 deposited under accession number ATCC 98887; or the nucleotide sequence of a mature protein coding sequence of clone yh50_1 deposited under
15 accession number ATCC 98887. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yh50_1 deposited under accession number ATCC 98887. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:124 having biological activity, the fragment
20 preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:124, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:124 having biological activity, the fragment comprising the amino acid sequence from amino acid 41 to amino acid 50 of SEQ ID NO:124.

25 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:123.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

30 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:123, but excluding the poly(A) tail at the 3' end of SEQ ID NO:123; and

- (ab) the nucleotide sequence of the cDNA insert of clone
yh50_1 deposited under accession number ATCC 98887;
- (ii) hybridizing said probe(s) to human genomic DNA in
conditions at least as stringent as 4X SSC at 50 degrees C; and
- 5 (iii) isolating the DNA polynucleotides detected with the
probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
10 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from
the group consisting of:
- (ba) SEQ ID NO:123, but excluding the poly(A) tail at the
3' end of SEQ ID NO:123; and
- (bb) the nucleotide sequence of the cDNA insert of clone
15 yh50_1 deposited under accession number ATCC 98887;
- (ii) hybridizing said primer(s) to human genomic DNA in
conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- 20 Preferably the polynucleotide isolated according to the above process comprises a
nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:123, and
extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ
ID NO:123 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:123, but
excluding the poly(A) tail at the 3' end of SEQ ID NO:123. Also preferably the
25 polynucleotide isolated according to the above process comprises a nucleotide sequence
corresponding to the cDNA sequence of SEQ ID NO:123 from nucleotide 127 to nucleotide
405, and extending contiguously from a nucleotide sequence corresponding to the 5' end
of said sequence of SEQ ID NO:123 from nucleotide 127 to nucleotide 405, to a nucleotide
sequence corresponding to the 3' end of said sequence of SEQ ID NO:123 from nucleotide
30 127 to nucleotide 405. Also preferably the polynucleotide isolated according to the above
process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID
NO:123 from nucleotide 268 to nucleotide 405, and extending contiguously from a
nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:123 from

nucleotide 268 to nucleotide 405, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:123 from nucleotide 268 to nucleotide 405.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group
5 consisting of:

- (a) the amino acid sequence of SEQ ID NO:124;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:124, the fragment comprising eight contiguous amino acids of SEQ ID NO:124; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone
10 yh50_1 deposited under accession number ATCC 98887;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:124. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:124 having biological activity, the fragment preferably
15 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:124, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:124 having biological activity, the fragment comprising the amino acid sequence from amino acid 41 to amino acid 50 of SEQ ID NO:124.

In one embodiment, the present invention provides a composition comprising an
20 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:125;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:125 from nucleotide 1175 to nucleotide 1480;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yh53_1 deposited under accession number ATCC 98887;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yh53_1 deposited under accession number ATCC 98887;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yh53_1 deposited under accession number ATCC
30 98887;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yh53_1 deposited under accession number ATCC 98887;

- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:126;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:126 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:126;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:125.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:125 from nucleotide 1175 to nucleotide 1480; the nucleotide sequence of the full-length protein coding sequence of clone yh53_1 deposited under accession number ATCC 98887; or the nucleotide sequence of a mature protein coding sequence of clone yh53_1 deposited under accession number ATCC 98887. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yh53_1 deposited under accession number ATCC 98887. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:126 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:126, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:126 having biological activity, the fragment comprising the amino acid sequence from amino acid 46 to amino acid 55 of SEQ ID NO:126.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:125.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:

- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- 5 (aa) SEQ ID NO:125, but excluding the poly(A) tail at the 3' end of SEQ ID NO:125; and
- (ab) the nucleotide sequence of the cDNA insert of clone yh53_1 deposited under accession number ATCC 98887;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 10 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 15 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:125, but excluding the poly(A) tail at the 3' end of SEQ ID NO:125; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 20 yh53_1 deposited under accession number ATCC 98887;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- 25 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:125, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:125 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:125, but excluding the poly(A) tail at the 3' end of SEQ ID NO:125. Also preferably the
- 30 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:125 from nucleotide 1175 to nucleotide 1480, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:125 from nucleotide 1175 to nucleotide 1480,

to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:125 from nucleotide 1175 to nucleotide 1480.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group

5 consisting of:

- (a) the amino acid sequence of SEQ ID NO:126;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:126, the fragment comprising eight contiguous amino acids of SEQ ID NO:126; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone
- 10 yh53_1 deposited under accession number ATCC 98887;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:126. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:126 having biological activity, the fragment preferably

15 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:126, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:126 having biological activity, the fragment comprising the amino acid sequence from amino acid 46 to amino acid 55 of SEQ ID NO:126.

In one embodiment, the present invention provides a composition comprising an

20 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:127;
 - (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:127 from nucleotide 65 to nucleotide 319;
 - (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
- 25 NO:127 from nucleotide 173 to nucleotide 319;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yh98_1 deposited under accession number ATCC 98887;
 - (e) a polynucleotide encoding the full-length protein encoded by the
- 30 cDNA insert of clone yh98_1 deposited under accession number ATCC 98887;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yh98_1 deposited under accession number ATCC 98887;

- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yh98_1 deposited under accession number ATCC 98887;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:128;
- 5 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:128 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:128;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- 10 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:127.
- 15

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:127 from nucleotide 65 to nucleotide 319; the nucleotide sequence of SEQ ID NO:127 from nucleotide 173 to nucleotide 319; the nucleotide sequence of the full-length protein coding sequence of clone yh98_1 deposited under accession number ATCC 98887; or the nucleotide sequence of a mature protein coding sequence of clone yh98_1 deposited under accession number ATCC 98887. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yh98_1 deposited under accession number ATCC 98887. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:128 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:128, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:128 having biological activity, the fragment comprising the amino acid sequence from amino acid 37 to amino acid 46 of SEQ ID NO:128.

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Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:127.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize
5 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:127, but excluding the poly(A) tail at the 3' end of SEQ ID NO:127; and
 - (ab) the nucleotide sequence of the cDNA insert of clone
10 yh98_1 deposited under accession number ATCC 98887;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);
- 15 and
- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - 20 (ba) SEQ ID NO:127, but excluding the poly(A) tail at the 3' end of SEQ ID NO:127; and
 - (bb) the nucleotide sequence of the cDNA insert of clone yh98_1 deposited under accession number ATCC 98887;
 - (ii) hybridizing said primer(s) to human genomic DNA in
25 conditions at least as stringent as 4X SSC at 50 degrees C;
 - (iii) amplifying human DNA sequences; and
 - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:127, and
30 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:127 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:127, but excluding the poly(A) tail at the 3' end of SEQ ID NO:127. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:127 from nucleotide 65 to nucleotide

319, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:127 from nucleotide 65 to nucleotide 319, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:127 from nucleotide 65 to nucleotide 319. Also preferably the polynucleotide isolated according to the above
5 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:127 from nucleotide 173 to nucleotide 319, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:127 from nucleotide 173 to nucleotide 319, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:127 from nucleotide 173 to nucleotide 319.

10 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:128;
- (b) a fragment of the amino acid sequence of SEQ ID NO:128, the
15 fragment comprising eight contiguous amino acids of SEQ ID NO:128; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yh98_1 deposited under accession number ATCC 98887;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:128. In further preferred
20 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:128 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:128, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:128 having biological activity, the fragment comprising the amino acid sequence
25 from amino acid 37 to amino acid 46 of SEQ ID NO:128.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:129;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID
30 NO:129 from nucleotide 122 to nucleotide 469;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:129 from nucleotide 263 to nucleotide 469;

- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ya69_1 deposited under accession number ATCC 98915;
- 5 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ya69_1 deposited under accession number ATCC 98915;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ya69_1 deposited under accession number ATCC 98915;
- 10 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ya69_1 deposited under accession number ATCC 98915;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:130;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:130 having biological activity, the fragment
- 15 comprising eight contiguous amino acids of SEQ ID NO:130;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 20 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:129.
- 25 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:129 from nucleotide 122 to nucleotide 469; the nucleotide sequence of SEQ ID NO:129 from nucleotide 263 to nucleotide 469; the nucleotide sequence of the full-length protein coding sequence of clone ya69_1 deposited under accession number ATCC 98915; or the nucleotide sequence of a mature protein coding sequence of clone ya69_1 deposited under
- 30 accession number ATCC 98915. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ya69_1 deposited under accession number ATCC 98915. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:130 having biological activity, the fragment

preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:130, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:130 having biological activity, the fragment comprising the amino acid sequence from amino acid 53 to amino acid 62 of SEQ ID NO:130.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:129.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 10 (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - 15 (aa) SEQ ID NO:129, but excluding the poly(A) tail at the 3' end of SEQ ID NO:129; and
 - (ab) the nucleotide sequence of the cDNA insert of clone ya69_1 deposited under accession number ATCC 98915;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - 20 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that
 - 25 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (ba) SEQ ID NO:129, but excluding the poly(A) tail at the 3' end of SEQ ID NO:129; and
 - (bb) the nucleotide sequence of the cDNA insert of clone
 - 30 ya69_1 deposited under accession number ATCC 98915;
 - (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
 - (iii) amplifying human DNA sequences; and
 - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:129, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:129 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:129, but
5 excluding the poly(A) tail at the 3' end of SEQ ID NO:129. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:129 from nucleotide 122 to nucleotide 469, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:129 from nucleotide 122 to nucleotide 469, to a nucleotide
10 sequence corresponding to the 3' end of said sequence of SEQ ID NO:129 from nucleotide 122 to nucleotide 469. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:129 from nucleotide 263 to nucleotide 469, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:129 from
15 nucleotide 263 to nucleotide 469, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:129 from nucleotide 263 to nucleotide 469.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 20 (a) the amino acid sequence of SEQ ID NO:130;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:130, the fragment comprising eight contiguous amino acids of SEQ ID NO:130; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone ya69_1 deposited under accession number ATCC 98915;
- 25 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:130. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:130 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
30 of SEQ ID NO:130, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:130 having biological activity, the fragment comprising the amino acid sequence from amino acid 53 to amino acid 62 of SEQ ID NO:130.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:131;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:131 from nucleotide 36 to nucleotide 554;
- 5 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:131 from nucleotide 183 to nucleotide 554;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yd107_1 deposited under accession number ATCC 98915;
- 10 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yd107_1 deposited under accession number ATCC 98915;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yd107_1 deposited under accession number ATCC 98915;
- 15 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yd107_1 deposited under accession number ATCC 98915;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:132;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:132 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:132;
- 20 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 25 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least
- 30 25% of the length of SEQ ID NO:131.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:131 from nucleotide 36 to nucleotide 554; the nucleotide sequence of SEQ ID NO:131 from nucleotide 183 to nucleotide 554; the nucleotide sequence of the full-length protein coding sequence of clone yd107_1 deposited under accession number ATCC 98915; or the

nucleotide sequence of a mature protein coding sequence of clone yd107_1 deposited under accession number ATCC 98915. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yd107_1 deposited under accession number ATCC 98915. In further preferred
5 embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:132 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:132, or a polynucleotide
10 having biological activity, the fragment comprising the amino acid sequence from amino acid 81 to amino acid 90 of SEQ ID NO:132.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:131.

Further embodiments of the invention provide isolated polynucleotides produced
15 according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

20 (aa) SEQ ID NO:131, but excluding the poly(A) tail at the 3' end of SEQ ID NO:131; and

(ab) the nucleotide sequence of the cDNA insert of clone yd107_1 deposited under accession number ATCC 98915;

25 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

30 (ba) SEQ ID NO:131, but excluding the poly(A) tail at the 3' end of SEQ ID NO:131; and

- (bb) the nucleotide sequence of the cDNA insert of clone yd107_1 deposited under accession number ATCC 98915;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 5 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:131, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:131 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:131, but excluding the poly(A) tail at the 3' end of SEQ ID NO:131. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:131 from nucleotide 36 to nucleotide 554, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:131 from nucleotide 36 to nucleotide 554, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:131 from nucleotide 36 to nucleotide 554. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:131 from nucleotide 183 to nucleotide 554, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:131 from nucleotide 183 to nucleotide 554, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:131 from nucleotide 183 to nucleotide 554.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:132;
- (b) a fragment of the amino acid sequence of SEQ ID NO:132, the fragment comprising eight contiguous amino acids of SEQ ID NO:132; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yd107_1 deposited under accession number ATCC 98915;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:132. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:132 having biological activity, the fragment preferably

comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:132, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:132 having biological activity, the fragment comprising the amino acid sequence from amino acid 81 to amino acid 90 of SEQ ID NO:132.

5 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:133;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID
10 NO:133 from nucleotide 8 to nucleotide 493;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:133 from nucleotide 53 to nucleotide 493;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yd145_1 deposited under accession
15 number ATCC 98915;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yd145_1 deposited under accession number ATCC 98915;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yd145_1 deposited under accession number
20 ATCC 98915;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yd145_1 deposited under accession number ATCC 98915;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:134;
- (i) a polynucleotide encoding a protein comprising a fragment of the
25 amino acid sequence of SEQ ID NO:134 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:134;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein
30 of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:133.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:133 from nucleotide 8 to nucleotide 493; the nucleotide sequence of SEQ ID NO:133 from nucleotide 53 to nucleotide 493; the nucleotide sequence of the full-length protein coding sequence of clone yd145_1 deposited under accession number ATCC 98915; or the nucleotide sequence of a mature protein coding sequence of clone yd145_1 deposited under accession number ATCC 98915. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yd145_1 deposited under accession number ATCC 98915. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:134 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:134, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:134 having biological activity, the fragment comprising the amino acid sequence from amino acid 76 to amino acid 85 of SEQ ID NO:134.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:133.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:133, but excluding the poly(A) tail at the 3' end of SEQ ID NO:133; and
 - (ab) the nucleotide sequence of the cDNA insert of clone yd145_1 deposited under accession number ATCC 98915;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:133, but excluding the poly(A) tail at the 3' end of SEQ ID NO:133; and

(bb) the nucleotide sequence of the cDNA insert of clone yd145_1 deposited under accession number ATCC 98915;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:133, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:133 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:133, but excluding the poly(A) tail at the 3' end of SEQ ID NO:133. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:133 from nucleotide 8 to nucleotide 493, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:133 from nucleotide 8 to nucleotide 493, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:133 from nucleotide 8 to nucleotide 493. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:133 from nucleotide 53 to nucleotide 493, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:133 from nucleotide 53 to nucleotide 493, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:133 from nucleotide 53 to nucleotide 493.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:134;

- (b) a fragment of the amino acid sequence of SEQ ID NO:134, the fragment comprising eight contiguous amino acids of SEQ ID NO:134; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yd145_1 deposited under accession number ATCC 98915;
- 5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:134. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:134 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 10 of SEQ ID NO:134, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:134 having biological activity, the fragment comprising the amino acid sequence from amino acid 76 to amino acid 85 of SEQ ID NO:134.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:135;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:135 from nucleotide 21 to nucleotide 308;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yh24_1 deposited under accession number
- 20 ATCC 98915;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yh24_1 deposited under accession number ATCC 98915;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yh24_1 deposited under accession number ATCC
- 25 98915;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yh24_1 deposited under accession number ATCC 98915;
- (g) a polynucleotide encoding a protein comprising the amino acid
- 30 sequence of SEQ ID NO:136;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:136 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:136;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

5 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:135.

10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:135 from nucleotide 21 to nucleotide 308; the nucleotide sequence of the full-length protein coding sequence of clone yh24_1 deposited under accession number ATCC 98915; or the nucleotide sequence of a mature protein coding sequence of clone yh24_1 deposited under accession number ATCC 98915. In other preferred embodiments, the
15 polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yh24_1 deposited under accession number ATCC 98915. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:136 having biological activity, the fragment preferably comprising eight (more preferably twenty, most
20 preferably thirty) contiguous amino acids of SEQ ID NO:136, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:136 having biological activity, the fragment comprising the amino acid sequence from amino acid 43 to amino acid 52 of SEQ ID NO:136.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ
25 ID NO:135.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize
30 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:135, but excluding the poly(A) tail at the 3' end of SEQ ID NO:135; and

- (ab) the nucleotide sequence of the cDNA insert of clone
yh24_1 deposited under accession number ATCC 98915;
- (ii) hybridizing said probe(s) to human genomic DNA in
conditions at least as stringent as 4X SSC at 50 degrees C; and
- 5 (iii) isolating the DNA polynucleotides detected with the
probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
10 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from
the group consisting of:
- (ba) SEQ ID NO:135, but excluding the poly(A) tail at the
3' end of SEQ ID NO:135; and
- (bb) the nucleotide sequence of the cDNA insert of clone
15 yh24_1 deposited under accession number ATCC 98915;
- (ii) hybridizing said primer(s) to human genomic DNA in
conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- 20 Preferably the polynucleotide isolated according to the above process comprises a
nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:135, and
extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ
ID NO:135 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:135, but
excluding the poly(A) tail at the 3' end of SEQ ID NO:135. Also preferably the
25 polynucleotide isolated according to the above process comprises a nucleotide sequence
corresponding to the cDNA sequence of SEQ ID NO:135 from nucleotide 21 to nucleotide
308, and extending contiguously from a nucleotide sequence corresponding to the 5' end
of said sequence of SEQ ID NO:135 from nucleotide 21 to nucleotide 308, to a nucleotide
sequence corresponding to the 3' end of said sequence of SEQ ID NO:135 from nucleotide
30 21 to nucleotide 308.

In other embodiments, the present invention provides a composition comprising
a protein, wherein said protein comprises an amino acid sequence selected from the group
consisting of:

- (a) the amino acid sequence of SEQ ID NO:136;

- (b) a fragment of the amino acid sequence of SEQ ID NO:136, the fragment comprising eight contiguous amino acids of SEQ ID NO:136; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yh24_1 deposited under accession number ATCC 98915;
- 5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:136. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:136 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 10 of SEQ ID NO:136, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:136 having biological activity, the fragment comprising the amino acid sequence from amino acid 43 to amino acid 52 of SEQ ID NO:136.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:137;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:137 from nucleotide 214 to nucleotide 735;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
- 20 NO:137 from nucleotide 634 to nucleotide 735;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yi11_1 deposited under accession number ATCC 98915;
- (e) a polynucleotide encoding the full-length protein encoded by the
- 25 cDNA insert of clone yi11_1 deposited under accession number ATCC 98915;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yi11_1 deposited under accession number ATCC 98915;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA
- 30 insert of clone yi11_1 deposited under accession number ATCC 98915;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:138;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:138 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:138;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:137.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:137 from nucleotide 214 to nucleotide 735; the nucleotide sequence of SEQ ID NO:137 from nucleotide 634 to nucleotide 735; the nucleotide sequence of the full-length protein coding sequence of clone yi11_1 deposited under accession number ATCC 98915; or the nucleotide sequence of a mature protein coding sequence of clone yi11_1 deposited under accession number ATCC 98915. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yi11_1 deposited under accession number ATCC 98915. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:138 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:138, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:138 having biological activity, the fragment comprising the amino acid sequence from amino acid 82 to amino acid 91 of SEQ ID NO:138.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:137.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:137, but excluding the poly(A) tail at the 3' end of SEQ ID NO:137; and

(ab) the nucleotide sequence of the cDNA insert of clone yi11_1 deposited under accession number ATCC 98915;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:137, but excluding the poly(A) tail at the 3' end of SEQ ID NO:137; and

(bb) the nucleotide sequence of the cDNA insert of clone yi11_1 deposited under accession number ATCC 98915;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:137, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:137 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:137, but excluding the poly(A) tail at the 3' end of SEQ ID NO:137. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:137 from nucleotide 214 to nucleotide 735, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:137 from nucleotide 214 to nucleotide 735, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:137 from nucleotide

214 to nucleotide 735. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:137 from nucleotide 634 to nucleotide 735, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:137 from
5 nucleotide 634 to nucleotide 735, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:137 from nucleotide 634 to nucleotide 735.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:138;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:138, the fragment comprising eight contiguous amino acids of SEQ ID NO:138; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone yi11_1 deposited under accession number ATCC 98915;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:138. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:138 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
20 of SEQ ID NO:138, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:138 having biological activity, the fragment comprising the amino acid sequence from amino acid 82 to amino acid 91 of SEQ ID NO:138.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:139;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:139 from nucleotide 668 to nucleotide 937;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
30 NO:139 from nucleotide 848 to nucleotide 937;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yi18_1 deposited under accession number ATCC 98915;

- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yi18_1 deposited under accession number ATCC 98915;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yi18_1 deposited under accession number ATCC 98915;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yi18_1 deposited under accession number ATCC 98915;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:140;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:140 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:140;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:139.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:139 from nucleotide 668 to nucleotide 937; the nucleotide sequence of SEQ ID NO:139 from nucleotide 848 to nucleotide 937; the nucleotide sequence of the full-length protein coding sequence of clone yi18_1 deposited under accession number ATCC 98915; or the nucleotide sequence of a mature protein coding sequence of clone yi18_1 deposited under accession number ATCC 98915. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yi18_1 deposited under accession number ATCC 98915. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:140 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:140, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:140 having biological activity, the

fragment comprising the amino acid sequence from amino acid 40 to amino acid 49 of SEQ ID NO:140.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:139.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

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(aa) SEQ ID NO:139, but excluding the poly(A) tail at the 3' end of SEQ ID NO:139; and

(ab) the nucleotide sequence of the cDNA insert of clone yi18_1 deposited under accession number ATCC 98915;

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(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25

(ba) SEQ ID NO:139, but excluding the poly(A) tail at the 3' end of SEQ ID NO:139; and

(bb) the nucleotide sequence of the cDNA insert of clone yi18_1 deposited under accession number ATCC 98915;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

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(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:139, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

ID NO:139 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:139, but excluding the poly(A) tail at the 3' end of SEQ ID NO:139. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:139 from nucleotide 668 to nucleotide 937, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:139 from nucleotide 668 to nucleotide 937, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:139 from nucleotide 668 to nucleotide 937. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:139 from nucleotide 848 to nucleotide 937, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:139 from nucleotide 848 to nucleotide 937, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:139 from nucleotide 848 to nucleotide 937.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:140;
- (b) a fragment of the amino acid sequence of SEQ ID NO:140, the fragment comprising eight contiguous amino acids of SEQ ID NO:140; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yi18_1 deposited under accession number ATCC 98915;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:140. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:140 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:140, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:140 having biological activity, the fragment comprising the amino acid sequence from amino acid 40 to amino acid 49 of SEQ ID NO:140.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:141;

- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:141 from nucleotide 171 to nucleotide 407;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:141 from nucleotide 258 to nucleotide 407;
- 5 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yk14_1 deposited under accession number ATCC 98915;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yk14_1 deposited under accession number ATCC 98915;
- 10 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yk14_1 deposited under accession number ATCC 98915;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yk14_1 deposited under accession number ATCC 98915;
- 15 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:142;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:142 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:142;
- 20 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 25 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:141.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:141 from nucleotide 171 to nucleotide 407; the nucleotide sequence of SEQ ID NO:141 from nucleotide 258 to nucleotide 407; the nucleotide sequence of the full-length protein coding sequence of clone yk14_1 deposited under accession number ATCC 98915; or the nucleotide sequence of a mature protein coding sequence of clone yk14_1 deposited under accession number ATCC 98915. In other preferred embodiments, the polynucleotide

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encodes the full-length or a mature protein encoded by the cDNA insert of clone yk14_1 deposited under accession number ATCC 98915. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:142 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:142, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:142 having biological activity, the fragment comprising the amino acid sequence from amino acid 34 to amino acid 43 of SEQ ID NO:142.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:141.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:141, but excluding the poly(A) tail at the 3' end of SEQ ID NO:141; and
 - (ab) the nucleotide sequence of the cDNA insert of clone yk14_1 deposited under accession number ATCC 98915;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (ba) SEQ ID NO:141, but excluding the poly(A) tail at the 3' end of SEQ ID NO:141; and
 - (bb) the nucleotide sequence of the cDNA insert of clone yk14_1 deposited under accession number ATCC 98915;

- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

5 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:141, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:141 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:141, but excluding the poly(A) tail at the 3' end of SEQ ID NO:141. Also preferably the
10 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:141 from nucleotide 171 to nucleotide 407, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:141 from nucleotide 171 to nucleotide 407, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:141 from nucleotide
15 171 to nucleotide 407. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:141 from nucleotide 258 to nucleotide 407, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:141 from nucleotide 258 to nucleotide 407, to a nucleotide sequence corresponding to the 3' end of
20 said sequence of SEQ ID NO:141 from nucleotide 258 to nucleotide 407.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:142;
- 25 (b) a fragment of the amino acid sequence of SEQ ID NO:142, the fragment comprising eight contiguous amino acids of SEQ ID NO:142; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yk14_1 deposited under accession number ATCC 98915;

the protein being substantially free from other mammalian proteins. Preferably such
30 protein comprises the amino acid sequence of SEQ ID NO:142. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:142 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:142, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:142 having biological activity, the fragment comprising the amino acid sequence from amino acid 34 to amino acid 43 of SEQ ID NO:142.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:143;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:143 from nucleotide 164 to nucleotide 457;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yk39_1 deposited under accession number
10 ATCC 98915;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yk39_1 deposited under accession number ATCC 98915;
- (e) a polynucleotide comprising the nucleotide sequence of a mature
15 protein coding sequence of clone yk39_1 deposited under accession number ATCC 98915;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yk39_1 deposited under accession number ATCC 98915;
- (g) a polynucleotide encoding a protein comprising the amino acid
20 sequence of SEQ ID NO:144;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:144 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:144;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of
25 (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:143.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:143 from nucleotide 164 to nucleotide 457; the nucleotide sequence of the full-length

protein coding sequence of clone yk39_1 deposited under accession number ATCC 98915; or the nucleotide sequence of a mature protein coding sequence of clone yk39_1 deposited under accession number ATCC 98915. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yk39_1 deposited under accession number ATCC 98915. In further preferred
5 embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:144 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:144, or a polynucleotide
10 encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:144 having biological activity, the fragment comprising the amino acid sequence from amino acid 44 to amino acid 53 of SEQ ID NO:144.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:143.

15 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:
(i) preparing one or more polynucleotide probes that hybridize
in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group
consisting of:

20 (aa) SEQ ID NO:143, but excluding the poly(A) tail at the 3' end of SEQ ID NO:143; and

(ab) the nucleotide sequence of the cDNA insert of clone yk39_1 deposited under accession number ATCC 98915;

25 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

30 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- (ba) SEQ ID NO:143, but excluding the poly(A) tail at the 3' end of SEQ ID NO:143; and
- (bb) the nucleotide sequence of the cDNA insert of clone yk39_1 deposited under accession number ATCC 98915;
- 5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:143, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:143 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:143, but excluding the poly(A) tail at the 3' end of SEQ ID NO:143. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence

10 corresponding to the cDNA sequence of SEQ ID NO:143 from nucleotide 164 to nucleotide 457, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:143 from nucleotide 164 to nucleotide 457, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:143 from nucleotide 164 to nucleotide 457.

20 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:144;
- (b) a fragment of the amino acid sequence of SEQ ID NO:144, the
- 25 fragment comprising eight contiguous amino acids of SEQ ID NO:144; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yk39_1 deposited under accession number ATCC 98915;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:144. In further preferred

30 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:144 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:144, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:144 having biological activity, the fragment comprising the amino acid sequence from amino acid 44 to amino acid 53 of SEQ ID NO:144.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:145;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:145 from nucleotide 72 to nucleotide 500;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
10 NO:145 from nucleotide 255 to nucleotide 500;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yk91_1 deposited under accession number ATCC 98915;
- (e) a polynucleotide encoding the full-length protein encoded by the
15 cDNA insert of clone yk91_1 deposited under accession number ATCC 98915;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yk91_1 deposited under accession number ATCC 98915;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA
20 insert of clone yk91_1 deposited under accession number ATCC 98915;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:146;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:146 having biological activity, the fragment
25 comprising eight contiguous amino acids of SEQ ID NO:146;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:145.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:145 from nucleotide 72 to nucleotide 500; the nucleotide sequence of SEQ ID NO:145 from nucleotide 255 to nucleotide 500; the nucleotide sequence of the full-length protein coding sequence of clone yk91_1 deposited under accession number ATCC 98915; or the
5 nucleotide sequence of a mature protein coding sequence of clone yk91_1 deposited under accession number ATCC 98915. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yk91_1 deposited under accession number ATCC 98915. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment
10 of the amino acid sequence of SEQ ID NO:146 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:146, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:146 having biological activity, the fragment comprising the amino acid sequence from amino acid 66 to amino acid 75 of SEQ
15 ID NO:146.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:145.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 20 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (aa) SEQ ID NO:145, but excluding the poly(A) tail at the
25 3' end of SEQ ID NO:145; and
- (ab) the nucleotide sequence of the cDNA insert of clone yk91_1 deposited under accession number ATCC 98915;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 30 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- 5 (ba) SEQ ID NO:145, but excluding the poly(A) tail at the 3' end of SEQ ID NO:145; and
- (bb) the nucleotide sequence of the cDNA insert of clone yk91_1 deposited under accession number ATCC 98915;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 10 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:145, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

15 ID NO:145 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:145, but excluding the poly(A) tail at the 3' end of SEQ ID NO:145. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:145 from nucleotide 72 to nucleotide 500, and extending contiguously from a nucleotide sequence corresponding to the 5' end

20 of said sequence of SEQ ID NO:145 from nucleotide 72 to nucleotide 500, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:145 from nucleotide 72 to nucleotide 500. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:145 from nucleotide 255 to nucleotide 500, and extending contiguously from a

25 nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:145 from nucleotide 255 to nucleotide 500, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:145 from nucleotide 255 to nucleotide 500.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group

30 consisting of:

- (a) the amino acid sequence of SEQ ID NO:146;
- (b) a fragment of the amino acid sequence of SEQ ID NO:146, the fragment comprising eight contiguous amino acids of SEQ ID NO:146; and

(c) the amino acid sequence encoded by the cDNA insert of clone yk91_1 deposited under accession number ATCC 98915; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:146. In further preferred
5 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:146 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:146, or a protein comprising a fragment of the amino acid sequence of SEQ
10 ID NO:146 having biological activity, the fragment comprising the amino acid sequence from amino acid 66 to amino acid 75 of SEQ ID NO:146.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:147;
- 15 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:147 from nucleotide 174 to nucleotide 620;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:147 from nucleotide 240 to nucleotide 620;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yk199_1 deposited under accession
20 number ATCC 98915;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yk199_1 deposited under accession number ATCC 98915;
- (f) a polynucleotide comprising the nucleotide sequence of a mature
25 protein coding sequence of clone yk199_1 deposited under accession number ATCC 98915;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yk199_1 deposited under accession number ATCC 98915;
- (h) a polynucleotide encoding a protein comprising the amino acid
30 sequence of SEQ ID NO:148;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:148 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:148;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

5 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:147.

10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:147 from nucleotide 174 to nucleotide 620; the nucleotide sequence of SEQ ID NO:147 from nucleotide 240 to nucleotide 620; the nucleotide sequence of the full-length protein coding sequence of clone yk199_1 deposited under accession number ATCC 98915; or the nucleotide sequence of a mature protein coding sequence of clone yk199_1 deposited
15 under accession number ATCC 98915. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yk199_1 deposited under accession number ATCC 98915. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:148 having biological
20 activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:148, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:148 having biological activity, the fragment comprising the amino acid sequence from amino acid 69 to amino acid 78 of SEQ ID NO:148.

25 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:147.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

30 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:147, but excluding the poly(A) tail at the 3' end of SEQ ID NO:147; and

- (ab) the nucleotide sequence of the cDNA insert of clone yk199_1 deposited under accession number ATCC 98915;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 5 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 10 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:147, but excluding the poly(A) tail at the 3' end of SEQ ID NO:147; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 15 yk199_1 deposited under accession number ATCC 98915;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- 20 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:147, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:147 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:147, but excluding the poly(A) tail at the 3' end of SEQ ID NO:147. Also preferably the
- 25 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:147 from nucleotide 174 to nucleotide 620, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:147 from nucleotide 174 to nucleotide 620, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:147 from nucleotide
- 30 174 to nucleotide 620. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:147 from nucleotide 240 to nucleotide 620, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:147 from

nucleotide 240 to nucleotide 620, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:147 from nucleotide 240 to nucleotide 620.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group
5 consisting of:

- (a) the amino acid sequence of SEQ ID NO:148;
- (b) a fragment of the amino acid sequence of SEQ ID NO:148, the fragment comprising eight contiguous amino acids of SEQ ID NO:148; and
- (c) the amino acid sequence encoded by the cDNA insert of clone
10 yk199_1 deposited under accession number ATCC 98915;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:148. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:148 having biological activity, the fragment preferably
15 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:148, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:148 having biological activity, the fragment comprising the amino acid sequence from amino acid 69 to amino acid 78 of SEQ ID NO:148.

In one embodiment, the present invention provides a composition comprising an
20 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:149;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:149 from nucleotide 325 to nucleotide 984;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
25 NO:149 from nucleotide 973 to nucleotide 984;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yl4_1 deposited under accession number ATCC 98915;
- (e) a polynucleotide encoding the full-length protein encoded by the
30 cDNA insert of clone yl4_1 deposited under accession number ATCC 98915;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yl4_1 deposited under accession number ATCC 98915;

- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yl4_1 deposited under accession number ATCC 98915;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:150;
- 5 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:150 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:150;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- 10 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:149.
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Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:149 from nucleotide 325 to nucleotide 984; the nucleotide sequence of SEQ ID NO:149 from nucleotide 973 to nucleotide 984; the nucleotide sequence of the full-length protein coding sequence of clone yl4_1 deposited under accession number ATCC 98915; or the nucleotide sequence of a mature protein coding sequence of clone yl4_1 deposited under accession number ATCC 98915. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yl4_1 deposited under accession number ATCC 98915. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:150 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:150, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:150 having biological activity, the fragment comprising the amino acid sequence from amino acid 105 to amino acid 114 of SEQ ID NO:150.

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Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:149.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:149, but excluding the poly(A) tail at the 3' end of SEQ ID NO:149; and

(ab) the nucleotide sequence of the cDNA insert of clone yl4_1 deposited under accession number ATCC 98915;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:149, but excluding the poly(A) tail at the 3' end of SEQ ID NO:149; and

(bb) the nucleotide sequence of the cDNA insert of clone yl4_1 deposited under accession number ATCC 98915;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:149, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:149 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:149, but excluding the poly(A) tail at the 3' end of SEQ ID NO:149. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:149 from nucleotide 325 to nucleotide

984, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:149 from nucleotide 325 to nucleotide 984, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:149 from nucleotide 325 to nucleotide 984. Also preferably the polynucleotide isolated according to the above
5 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:149 from nucleotide 973 to nucleotide 984, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:149 from nucleotide 973 to nucleotide 984, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:149 from nucleotide 973 to nucleotide 984.

10 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:150;
- (b) a fragment of the amino acid sequence of SEQ ID NO:150, the
15 fragment comprising eight contiguous amino acids of SEQ ID NO:150; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yl4_1 deposited under accession number ATCC 98915;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:150. In further preferred
20 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:150 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:150, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:150 having biological activity, the fragment comprising the amino acid sequence
25 from amino acid 105 to amino acid 114 of SEQ ID NO:150.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:151;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID
30 NO:151 from nucleotide 119 to nucleotide 415;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yl14_1 deposited under accession number ATCC 98915;

- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yl14_1 deposited under accession number ATCC 98915;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yl14_1 deposited under accession number ATCC 98915;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yl14_1 deposited under accession number ATCC 98915;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:152;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:152 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:152;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:151.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:151 from nucleotide 119 to nucleotide 415; the nucleotide sequence of the full-length protein coding sequence of clone yl14_1 deposited under accession number ATCC 98915; or the nucleotide sequence of a mature protein coding sequence of clone yl14_1 deposited under accession number ATCC 98915. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yl14_1 deposited under accession number ATCC 98915. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:152 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:152, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:152

having biological activity, the fragment comprising the amino acid sequence from amino acid 44 to amino acid 53 of SEQ ID NO:152.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:151.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

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(aa) SEQ ID NO:151, but excluding the poly(A) tail at the 3' end of SEQ ID NO:151; and

(ab) the nucleotide sequence of the cDNA insert of clone yl14_1 deposited under accession number ATCC 98915;

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(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

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(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

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(ba) SEQ ID NO:151, but excluding the poly(A) tail at the 3' end of SEQ ID NO:151; and

(bb) the nucleotide sequence of the cDNA insert of clone yl14_1 deposited under accession number ATCC 98915;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

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(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:151, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

ID NO:151 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:151, but excluding the poly(A) tail at the 3' end of SEQ ID NO:151. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:151 from nucleotide 119 to nucleotide 415, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:151 from nucleotide 119 to nucleotide 415, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:151 from nucleotide 119 to nucleotide 415.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:152;
- (b) a fragment of the amino acid sequence of SEQ ID NO:152, the fragment comprising eight contiguous amino acids of SEQ ID NO:152; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yl14_1 deposited under accession number ATCC 98915;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:152. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:152 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:152, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:152 having biological activity, the fragment comprising the amino acid sequence from amino acid 44 to amino acid 53 of SEQ ID NO:152.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:153;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:153 from nucleotide 96 to nucleotide 377;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:153 from nucleotide 225 to nucleotide 377;

- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ya80_1 deposited under accession number ATCC 98925;
- 5 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ya80_1 deposited under accession number ATCC 98925;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ya80_1 deposited under accession number ATCC 98925;
- 10 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ya80_1 deposited under accession number ATCC 98925;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:154;
- 15 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:154 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:154;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 20 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:153.
- 25 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:153 from nucleotide 96 to nucleotide 377; the nucleotide sequence of SEQ ID NO:153 from nucleotide 225 to nucleotide 377; the nucleotide sequence of the full-length protein coding sequence of clone ya80_1 deposited under accession number ATCC 98925; or the nucleotide sequence of a mature protein coding sequence of clone ya80_1 deposited under
- 30 accession number ATCC 98925. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ya80_1 deposited under accession number ATCC 98925. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:154 having biological activity, the fragment

preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:154, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:154 having biological activity, the fragment comprising the amino acid sequence from amino acid 42 to amino acid 51 of SEQ ID NO:154.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:153.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 10 (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - 15 (aa) SEQ ID NO:153, but excluding the poly(A) tail at the 3' end of SEQ ID NO:153; and
 - (ab) the nucleotide sequence of the cDNA insert of clone ya80_1 deposited under accession number ATCC 98925;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - 20 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that
 - 25 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (ba) SEQ ID NO:153, but excluding the poly(A) tail at the 3' end of SEQ ID NO:153; and
 - (bb) the nucleotide sequence of the cDNA insert of clone
 - 30 ya80_1 deposited under accession number ATCC 98925;
 - (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
 - (iii) amplifying human DNA sequences; and
 - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:153, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:153 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:153, but
5 excluding the poly(A) tail at the 3' end of SEQ ID NO:153. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:153 from nucleotide 96 to nucleotide 377, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:153 from nucleotide 96 to nucleotide 377, to a nucleotide
10 sequence corresponding to the 3' end of said sequence of SEQ ID NO:153 from nucleotide 96 to nucleotide 377. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:153 from nucleotide 225 to nucleotide 377, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:153 from
15 nucleotide 225 to nucleotide 377, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:153 from nucleotide 225 to nucleotide 377.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 20 (a) the amino acid sequence of SEQ ID NO:154;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:154, the fragment comprising eight contiguous amino acids of SEQ ID NO:154; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone ya80_1 deposited under accession number ATCC 98925;
- 25 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:154. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:154 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
30 of SEQ ID NO:154, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:154 having biological activity, the fragment comprising the amino acid sequence from amino acid 42 to amino acid 51 of SEQ ID NO:154.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:155;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:155 from nucleotide 118 to nucleotide 681;
- 5 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:155 from nucleotide 622 to nucleotide 681;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yd61_1 deposited under accession number ATCC 98925;
- 10 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yd61_1 deposited under accession number ATCC 98925;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yd61_1 deposited under accession number ATCC 98925;
- 15 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yd61_1 deposited under accession number ATCC 98925;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:156;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:156 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:156;
- 20 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 25 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:155.
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Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:155 from nucleotide 118 to nucleotide 681; the nucleotide sequence of SEQ ID NO:155 from nucleotide 622 to nucleotide 681; the nucleotide sequence of the full-length protein coding sequence of clone yd61_1 deposited under accession number ATCC 98925; or the

nucleotide sequence of a mature protein coding sequence of clone yd61_1 deposited under accession number ATCC 98925. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yd61_1 deposited under accession number ATCC 98925. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:156 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:156, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:156 having biological activity, the fragment comprising the amino acid sequence from amino acid 89 to amino acid 98 of SEQ ID NO:156.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:155.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- (aa) SEQ ID NO:155, but excluding the poly(A) tail at the 3' end of SEQ ID NO:155; and

- (ab) the nucleotide sequence of the cDNA insert of clone yd61_1 deposited under accession number ATCC 98925;

- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

- (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- (ba) SEQ ID NO:155, but excluding the poly(A) tail at the 3' end of SEQ ID NO:155; and

- (bb) the nucleotide sequence of the cDNA insert of clone yd61_1 deposited under accession number ATCC 98925;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 5 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:155, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:155 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:155, but excluding the poly(A) tail at the 3' end of SEQ ID NO:155. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:155 from nucleotide 118 to nucleotide 681, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:155 from nucleotide 118 to nucleotide 681, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:155 from nucleotide 118 to nucleotide 681. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:155 from nucleotide 622 to nucleotide 681, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:155 from nucleotide 622 to nucleotide 681, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:155 from nucleotide 622 to nucleotide 681.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 25 (a) the amino acid sequence of SEQ ID NO:156;
- (b) a fragment of the amino acid sequence of SEQ ID NO:156, the fragment comprising eight contiguous amino acids of SEQ ID NO:156; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yd61_1 deposited under accession number ATCC 98925;
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the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:156. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:156 having biological activity, the fragment preferably

comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:156, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:156 having biological activity, the fragment comprising the amino acid sequence from amino acid 89 to amino acid 98 of SEQ ID NO:156.

5 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:157;
- 10 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:157 from nucleotide 261 to nucleotide 614;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yd88_1 deposited under accession number ATCC 98925;
- 15 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yd88_1 deposited under accession number ATCC 98925;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yd88_1 deposited under accession number ATCC 98925;
- 20 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yd88_1 deposited under accession number ATCC 98925;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:158;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:158 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:158;
- 25 (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- 30 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:157.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:157 from nucleotide 261 to nucleotide 614; the nucleotide sequence of the full-length protein coding sequence of clone yd88_1 deposited under accession number ATCC 98925; or the nucleotide sequence of a mature protein coding sequence of clone yd88_1 deposited
5 under accession number ATCC 98925. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yd88_1 deposited under accession number ATCC 98925. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:158 having biological
10 activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:158, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:158 having biological activity, the fragment comprising the amino acid sequence from amino acid 54 to amino acid 63 of SEQ ID NO:158.

15 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:157.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - 20 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:157, but excluding the poly(A) tail at the 3' end of SEQ ID NO:157; and
 - 25 (ab) the nucleotide sequence of the cDNA insert of clone yd88_1 deposited under accession number ATCC 98925;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the
30 probe(s);

and

- (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- 5 (ba) SEQ ID NO:157, but excluding the poly(A) tail at the 3' end of SEQ ID NO:157; and
- (bb) the nucleotide sequence of the cDNA insert of clone yd88_1 deposited under accession number ATCC 98925;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 10 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:157, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

15 ID NO:157 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:157, but excluding the poly(A) tail at the 3' end of SEQ ID NO:157. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:157 from nucleotide 261 to nucleotide 614, and extending contiguously from a nucleotide sequence corresponding to the 5' end

20 of said sequence of SEQ ID NO:157 from nucleotide 261 to nucleotide 614, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:157 from nucleotide 261 to nucleotide 614.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group

25 consisting of:

- (a) the amino acid sequence of SEQ ID NO:158;
- (b) a fragment of the amino acid sequence of SEQ ID NO:158, the fragment comprising eight contiguous amino acids of SEQ ID NO:158; and
- (c) the amino acid sequence encoded by the cDNA insert of clone
- 30 yd88_1 deposited under accession number ATCC 98925;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:158. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:158 having biological activity, the fragment preferably

comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:158, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:158 having biological activity, the fragment comprising the amino acid sequence from amino acid 54 to amino acid 63 of SEQ ID NO:158.

5 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:159;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID
10 NO:159 from nucleotide 26 to nucleotide 475;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yd109_1 deposited under accession number ATCC 98925;
- (d) a polynucleotide encoding the full-length protein encoded by the
15 cDNA insert of clone yd109_1 deposited under accession number ATCC 98925;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yd109_1 deposited under accession number ATCC 98925;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA
20 insert of clone yd109_1 deposited under accession number ATCC 98925;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:160;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:160 having biological activity, the fragment
25 comprising eight contiguous amino acids of SEQ ID NO:160;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any
30 one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:159.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:159 from nucleotide 26 to nucleotide 475; the nucleotide sequence of the full-length protein coding sequence of clone yd109_1 deposited under accession number ATCC 98925; or the nucleotide sequence of a mature protein coding sequence of clone yd109_1 deposited under accession number ATCC 98925. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yd109_1 deposited under accession number ATCC 98925. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:160 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:160, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:160 having biological activity, the fragment comprising the amino acid sequence from amino acid 70 to amino acid 79 of SEQ ID NO:160.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:159.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:159, but excluding the poly(A) tail at the 3' end of SEQ ID NO:159; and
 - (ab) the nucleotide sequence of the cDNA insert of clone yd109_1 deposited under accession number ATCC 98925;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- 5 (ba) SEQ ID NO:159, but excluding the poly(A) tail at the 3' end of SEQ ID NO:159; and
- (bb) the nucleotide sequence of the cDNA insert of clone yd109_1 deposited under accession number ATCC 98925;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 10 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:159, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

15 ID NO:159 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:159, but excluding the poly(A) tail at the 3' end of SEQ ID NO:159. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:159 from nucleotide 26 to nucleotide 475, and extending contiguously from a nucleotide sequence corresponding to the 5' end

20 of said sequence of SEQ ID NO:159 from nucleotide 26 to nucleotide 475, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:159 from nucleotide 26 to nucleotide 475.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group

25 consisting of:

- (a) the amino acid sequence of SEQ ID NO:160;
- (b) a fragment of the amino acid sequence of SEQ ID NO:160, the fragment comprising eight contiguous amino acids of SEQ ID NO:160; and
- (c) the amino acid sequence encoded by the cDNA insert of clone
- 30 yd109_1 deposited under accession number ATCC 98925;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:160. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:160 having biological activity, the fragment preferably

comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:160, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:160 having biological activity, the fragment comprising the amino acid sequence from amino acid 70 to amino acid 79 of SEQ ID NO:160.

5 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:161;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID
10 NO:161 from nucleotide 79 to nucleotide 474;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yd141_1 deposited under accession number ATCC 98925;
- (d) a polynucleotide encoding the full-length protein encoded by the
15 cDNA insert of clone yd141_1 deposited under accession number ATCC 98925;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yd141_1 deposited under accession number ATCC 98925;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA
20 insert of clone yd141_1 deposited under accession number ATCC 98925;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:162;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:162 having biological activity, the fragment
25 comprising eight contiguous amino acids of SEQ ID NO:162;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any
30 one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:161.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:161 from nucleotide 79 to nucleotide 474; the nucleotide sequence of the full-length protein coding sequence of clone yd141_1 deposited under accession number ATCC 98925; or the nucleotide sequence of a mature protein coding sequence of clone yd141_1 deposited under accession number ATCC 98925. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yd141_1 deposited under accession number ATCC 98925. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:162 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:162, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:162 having biological activity, the fragment comprising the amino acid sequence from amino acid 61 to amino acid 70 of SEQ ID NO:162.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:161.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:161, but excluding the poly(A) tail at the 3' end of SEQ ID NO:161; and
 - (ab) the nucleotide sequence of the cDNA insert of clone yd141_1 deposited under accession number ATCC 98925;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- 5 (ba) SEQ ID NO:161, but excluding the poly(A) tail at the 3' end of SEQ ID NO:161; and
- (bb) the nucleotide sequence of the cDNA insert of clone yd141_1 deposited under accession number ATCC 98925;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 10 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:161, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:161 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:161, but excluding the poly(A) tail at the 3' end of SEQ ID NO:161. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:161 from nucleotide 79 to nucleotide 474, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:161 from nucleotide 79 to nucleotide 474, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:161 from nucleotide 79 to nucleotide 474.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 25 (a) the amino acid sequence of SEQ ID NO:162;
- (b) a fragment of the amino acid sequence of SEQ ID NO:162, the fragment comprising eight contiguous amino acids of SEQ ID NO:162; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yd141_1 deposited under accession number ATCC 98925;
- 30

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:162. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:162 having biological activity, the fragment preferably

comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:162, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:162 having biological activity, the fragment comprising the amino acid sequence from amino acid 61 to amino acid 70 of SEQ ID NO:162.

5 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:163;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID
10 NO:163 from nucleotide 45 to nucleotide 347;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:163 from nucleotide 135 to nucleotide 347;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yd153_1 deposited under accession
15 number ATCC 98925;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yd153_1 deposited under accession number ATCC 98925;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yd153_1 deposited under accession number
20 ATCC 98925;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yd153_1 deposited under accession number ATCC 98925;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:164;
- (i) a polynucleotide encoding a protein comprising a fragment of the
25 amino acid sequence of SEQ ID NO:164 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:164;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein
30 of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:163.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:163 from nucleotide 45 to nucleotide 347; the nucleotide sequence of SEQ ID NO:163 from nucleotide 135 to nucleotide 347; the nucleotide sequence of the full-length protein coding sequence of clone yd153_1 deposited under accession number ATCC 98925; or the nucleotide sequence of a mature protein coding sequence of clone yd153_1 deposited under accession number ATCC 98925. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yd153_1 deposited under accession number ATCC 98925. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:164 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:164, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:164 having biological activity, the fragment comprising the amino acid sequence from amino acid 45 to amino acid 54 of SEQ ID NO:164.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:163.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:163, but excluding the poly(A) tail at the 3' end of SEQ ID NO:163; and
 - (ab) the nucleotide sequence of the cDNA insert of clone yd153_1 deposited under accession number ATCC 98925;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:163, but excluding the poly(A) tail at the 3' end of SEQ ID NO:163; and

(bb) the nucleotide sequence of the cDNA insert of clone yd153_1 deposited under accession number ATCC 98925;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:163, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:163 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:163, but excluding the poly(A) tail at the 3' end of SEQ ID NO:163. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:163 from nucleotide 45 to nucleotide 347, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:163 from nucleotide 45 to nucleotide 347, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:163 from nucleotide 45 to nucleotide 347. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:163 from nucleotide 135 to nucleotide 347, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:163 from nucleotide 135 to nucleotide 347, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:163 from nucleotide 135 to nucleotide 347.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:164;

(b) a fragment of the amino acid sequence of SEQ ID NO:164, the fragment comprising eight contiguous amino acids of SEQ ID NO:164; and

(c) the amino acid sequence encoded by the cDNA insert of clone yd153_1 deposited under accession number ATCC 98925;

5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:164. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:164 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
10 of SEQ ID NO:164, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:164 having biological activity, the fragment comprising the amino acid sequence from amino acid 45 to amino acid 54 of SEQ ID NO:164.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:165;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:165 from nucleotide 114 to nucleotide 470;

20 (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yd165_1 deposited under accession number ATCC 98925;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yd165_1 deposited under accession number ATCC 98925;

25 (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yd165_1 deposited under accession number ATCC 98925;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yd165_1 deposited under accession number ATCC 98925;

30 (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:166;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:166 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:166;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

5 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:165.

10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:165 from nucleotide 114 to nucleotide 470; the nucleotide sequence of the full-length protein coding sequence of clone yd165_1 deposited under accession number ATCC 98925; or the nucleotide sequence of a mature protein coding sequence of clone yd165_1 deposited under accession number ATCC 98925. In other preferred embodiments, the
15 polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yd165_1 deposited under accession number ATCC 98925. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:166 having biological activity, the fragment preferably comprising eight (more preferably twenty, most
20 preferably thirty) contiguous amino acids of SEQ ID NO:166, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:166 having biological activity, the fragment comprising the amino acid sequence from amino acid 54 to amino acid 63 of SEQ ID NO:166.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ
25 ID NO:165.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

30 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:165, but excluding the poly(A) tail at the 3' end of SEQ ID NO:165; and

- (ab) the nucleotide sequence of the cDNA insert of clone yd165_1 deposited under accession number ATCC 98925;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - 5 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that
 - 10 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (ba) SEQ ID NO:165, but excluding the poly(A) tail at the 3' end of SEQ ID NO:165; and
 - (bb) the nucleotide sequence of the cDNA insert of clone
 - 15 yd165_1 deposited under accession number ATCC 98925;
 - (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
 - (iii) amplifying human DNA sequences; and
 - (iv) isolating the polynucleotide products of step (b)(iii).
- 20 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:165, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:165 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:165, but excluding the poly(A) tail at the 3' end of SEQ ID NO:165. Also preferably the
- 25 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:165 from nucleotide 114 to nucleotide 470, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:165 from nucleotide 114 to nucleotide 470, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:165 from nucleotide
- 30 114 to nucleotide 470.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:166;

- (b) a fragment of the amino acid sequence of SEQ ID NO:166, the fragment comprising eight contiguous amino acids of SEQ ID NO:166; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yd165_1 deposited under accession number ATCC 98925;
- 5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:166. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:166 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 10 of SEQ ID NO:166, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:166 having biological activity, the fragment comprising the amino acid sequence from amino acid 54 to amino acid 63 of SEQ ID NO:166.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:167;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:167 from nucleotide 82 to nucleotide 663;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
- 20 NO:167 from nucleotide 139 to nucleotide 663;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yd178_1 deposited under accession number ATCC 98925;
- (e) a polynucleotide encoding the full-length protein encoded by the
- 25 cDNA insert of clone yd178_1 deposited under accession number ATCC 98925;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yd178_1 deposited under accession number ATCC 98925;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA
- 30 insert of clone yd178_1 deposited under accession number ATCC 98925;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:168;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:168 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:168;

5 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

10 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:167.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:167 from nucleotide 82 to nucleotide 663; the nucleotide sequence of SEQ ID NO:167
15 from nucleotide 139 to nucleotide 663; the nucleotide sequence of the full-length protein coding sequence of clone yd178_1 deposited under accession number ATCC 98925; or the nucleotide sequence of a mature protein coding sequence of clone yd178_1 deposited under accession number ATCC 98925. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert
20 of clone yd178_1 deposited under accession number ATCC 98925. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:168 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:168, or a polynucleotide
25 encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:168 having biological activity, the fragment comprising the amino acid sequence from amino acid 92 to amino acid 101 of SEQ ID NO:168.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:167.

30 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:167, but excluding the poly(A) tail at the 3' end of SEQ ID NO:167; and

(ab) the nucleotide sequence of the cDNA insert of clone yd178_1 deposited under accession number ATCC 98925;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:167, but excluding the poly(A) tail at the 3' end of SEQ ID NO:167; and

(bb) the nucleotide sequence of the cDNA insert of clone yd178_1 deposited under accession number ATCC 98925;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:167, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:167 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:167, but excluding the poly(A) tail at the 3' end of SEQ ID NO:167. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:167 from nucleotide 82 to nucleotide 663, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:167 from nucleotide 82 to nucleotide 663, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:167 from nucleotide

82 to nucleotide 663. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:167 from nucleotide 139 to nucleotide 663, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:167 from
5 nucleotide 139 to nucleotide 663, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:167 from nucleotide 139 to nucleotide 663.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:168;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:168, the fragment comprising eight contiguous amino acids of SEQ ID NO:168; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone yd178_1 deposited under accession number ATCC 98925;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:168. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:168 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
20 of SEQ ID NO:168, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:168 having biological activity, the fragment comprising the amino acid sequence from amino acid 92 to amino acid 101 of SEQ ID NO:168.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:169;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:169 from nucleotide 121 to nucleotide 450;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yd191_1 deposited under accession
30 number ATCC 98925;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yd191_1 deposited under accession number ATCC 98925;

- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yd191_1 deposited under accession number ATCC 98925;
- 5 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yd191_1 deposited under accession number ATCC 98925;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:170;
- 10 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:170 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:170;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- 15 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:169.
- 20 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:169 from nucleotide 121 to nucleotide 450; the nucleotide sequence of the full-length protein coding sequence of clone yd191_1 deposited under accession number ATCC 98925; or the nucleotide sequence of a mature protein coding sequence of clone yd191_1 deposited under accession number ATCC 98925. In other preferred embodiments, the
- 25 polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yd191_1 deposited under accession number ATCC 98925. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:170 having biological activity, the fragment preferably comprising eight (more preferably twenty, most
- 30 preferably thirty) contiguous amino acids of SEQ ID NO:170, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:170 having biological activity, the fragment comprising the amino acid sequence from amino acid 50 to amino acid 59 of SEQ ID NO:170.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:169.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 5 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- 10 (aa) SEQ ID NO:169, but excluding the poly(A) tail at the 3' end of SEQ ID NO:169; and
- (ab) the nucleotide sequence of the cDNA insert of clone yd191_1 deposited under accession number ATCC 98925;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 15 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 20 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:169, but excluding the poly(A) tail at the 3' end of SEQ ID NO:169; and
- (bb) the nucleotide sequence of the cDNA insert of clone yd191_1 deposited under accession number ATCC 98925;
- 25 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- 30 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:169, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:169 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:169, but excluding the poly(A) tail at the 3' end of SEQ ID NO:169. Also preferably the

polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:169 from nucleotide 121 to nucleotide 450, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:169 from nucleotide 121 to nucleotide 450, to a nucleotide
5 sequence corresponding to the 3' end of said sequence of SEQ ID NO:169 from nucleotide 121 to nucleotide 450.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:170;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:170, the fragment comprising eight contiguous amino acids of SEQ ID NO:170; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone yd191_1 deposited under accession number ATCC 98925;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:170. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:170 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
20 of SEQ ID NO:170, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:170 having biological activity, the fragment comprising the amino acid sequence from amino acid 50 to amino acid 59 of SEQ ID NO:170.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:171;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:171 from nucleotide 33 to nucleotide 494;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ye7_1 deposited under accession number
30 ATCC 98924;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ye7_1 deposited under accession number ATCC 98924;

- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ye7_1 deposited under accession number ATCC 98924;
- 5 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ye7_1 deposited under accession number ATCC 98924;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:172;
- 10 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:172 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:172;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- 15 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:171.
- 20 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:171 from nucleotide 33 to nucleotide 494; the nucleotide sequence of the full-length protein coding sequence of clone ye7_1 deposited under accession number ATCC 98924; or the nucleotide sequence of a mature protein coding sequence of clone ye7_1 deposited under accession number ATCC 98924. In other preferred embodiments, the
- 25 polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ye7_1 deposited under accession number ATCC 98924. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:172 having biological activity, the fragment preferably comprising eight (more preferably twenty, most
- 30 preferably thirty) contiguous amino acids of SEQ ID NO:172, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:172 having biological activity, the fragment comprising the amino acid sequence from amino acid 72 to amino acid 81 of SEQ ID NO:172.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:171.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 5 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- 10 (aa) SEQ ID NO:171, but excluding the poly(A) tail at the 3' end of SEQ ID NO:171; and
- (ab) the nucleotide sequence of the cDNA insert of clone ye7_1 deposited under accession number ATCC 98924;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 15 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 20 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:171, but excluding the poly(A) tail at the 3' end of SEQ ID NO:171; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 25 ye7_1 deposited under accession number ATCC 98924;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

- 30 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:171, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:171 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:171, but excluding the poly(A) tail at the 3' end of SEQ ID NO:171. Also preferably the

polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:171 from nucleotide 33 to nucleotide 494, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:171 from nucleotide 33 to nucleotide 494, to a nucleotide
5 sequence corresponding to the 3' end of said sequence of SEQ ID NO:171 from nucleotide 33 to nucleotide 494.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:172;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:172, the fragment comprising eight contiguous amino acids of SEQ ID NO:172; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone ye7_1 deposited under accession number ATCC 98924;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:172. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:172 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
20 of SEQ ID NO:172, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:172 having biological activity, the fragment comprising the amino acid sequence from amino acid 72 to amino acid 81 of SEQ ID NO:172.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:173;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:173 from nucleotide 1251 to nucleotide 1625;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
30 NO:173 from nucleotide 1395 to nucleotide 1625;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yf33_1 deposited under accession number ATCC 98924;

- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yf33_1 deposited under accession number ATCC 98924;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yf33_1 deposited under accession number ATCC 98924;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yf33_1 deposited under accession number ATCC 98924;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:174;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:174 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:174;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:173.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:173 from nucleotide 1251 to nucleotide 1625; the nucleotide sequence of SEQ ID NO:173 from nucleotide 1395 to nucleotide 1625; the nucleotide sequence of the full-length protein coding sequence of clone yf33_1 deposited under accession number ATCC 98924; or the nucleotide sequence of a mature protein coding sequence of clone yf33_1 deposited under accession number ATCC 98924. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yf33_1 deposited under accession number ATCC 98924. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:174 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:174, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:174

having biological activity, the fragment comprising the amino acid sequence from amino acid 57 to amino acid 66 of SEQ ID NO:174.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:173.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

10 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:173, but excluding the poly(A) tail at the 3' end of SEQ ID NO:173; and

(ab) the nucleotide sequence of the cDNA insert of clone yf33_1 deposited under accession number ATCC 98924;

15 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25 (ba) SEQ ID NO:173, but excluding the poly(A) tail at the 3' end of SEQ ID NO:173; and

(bb) the nucleotide sequence of the cDNA insert of clone yf33_1 deposited under accession number ATCC 98924;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

30 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:173, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

ID NO:173 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:173, but excluding the poly(A) tail at the 3' end of SEQ ID NO:173. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:173 from nucleotide 1251 to nucleotide 1625, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:173 from nucleotide 1251 to nucleotide 1625, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:173 from nucleotide 1251 to nucleotide 1625. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:173 from nucleotide 1395 to nucleotide 1625, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:173 from nucleotide 1395 to nucleotide 1625, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:173 from nucleotide 1395 to nucleotide 1625.

15 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:174;
- (b) a fragment of the amino acid sequence of SEQ ID NO:174, the
20 fragment comprising eight contiguous amino acids of SEQ ID NO:174; and
- (c) the amino acid sequence encoded by the cDNA insert of clone
yf33_1 deposited under accession number ATCC 98924;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:174. In further preferred
25 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:174 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:174, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:174 having biological activity, the fragment comprising the amino acid sequence
30 from amino acid 57 to amino acid 66 of SEQ ID NO:174.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:175;

- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:175 from nucleotide 1299 to nucleotide 1640;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yi15_1 deposited under accession number ATCC 98924;
- 5 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yi15_1 deposited under accession number ATCC 98924;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yi15_1 deposited under accession number ATCC 98924;
- 10 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yi15_1 deposited under accession number ATCC 98924;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:176;
- 15 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:176 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:176;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- 20 (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:175.
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Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:175 from nucleotide 1299 to nucleotide 1640; the nucleotide sequence of the full-length protein coding sequence of clone yi15_1 deposited under accession number ATCC 98924; or the nucleotide sequence of a mature protein coding sequence of clone yi15_1 deposited under accession number ATCC 98924. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yi15_1 deposited under accession number ATCC 98924. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein

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comprising a fragment of the amino acid sequence of SEQ ID NO:176 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:176, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:176
5 having biological activity, the fragment comprising the amino acid sequence from amino acid 52 to amino acid 61 of SEQ ID NO:176.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:175.

Further embodiments of the invention provide isolated polynucleotides produced
10 according to a process selected from the group consisting of:

(a) a process comprising the steps of:
(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

15 (aa) SEQ ID NO:175, but excluding the poly(A) tail at the 3' end of SEQ ID NO:175; and

(ab) the nucleotide sequence of the cDNA insert of clone yi15_1 deposited under accession number ATCC 98924;

(ii) hybridizing said probe(s) to human genomic DNA in
20 conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

25 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:175, but excluding the poly(A) tail at the 3' end of SEQ ID NO:175; and

30 (bb) the nucleotide sequence of the cDNA insert of clone yi15_1 deposited under accession number ATCC 98924;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:175, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:175 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:175, but excluding the poly(A) tail at the 3' end of SEQ ID NO:175. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:175 from nucleotide 1299 to nucleotide 1640, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:175 from nucleotide 1299 to nucleotide 1640, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:175 from nucleotide 1299 to nucleotide 1640.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:176;
- (b) a fragment of the amino acid sequence of SEQ ID NO:176, the fragment comprising eight contiguous amino acids of SEQ ID NO:176; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yi15_1 deposited under accession number ATCC 98924;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:176. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:176 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:176, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:176 having biological activity, the fragment comprising the amino acid sequence from amino acid 52 to amino acid 61 of SEQ ID NO:176.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:177;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:177 from nucleotide 85 to nucleotide 1377;

- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:177 from nucleotide 139 to nucleotide 1377;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yi17_1 deposited under accession number ATCC 98924;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yi17_1 deposited under accession number ATCC 98924;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yi17_1 deposited under accession number ATCC 98924;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yi17_1 deposited under accession number ATCC 98924;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:178;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:178 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:178;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:177.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:177 from nucleotide 85 to nucleotide 1377; the nucleotide sequence of SEQ ID NO:177 from nucleotide 139 to nucleotide 1377; the nucleotide sequence of the full-length protein coding sequence of clone yi17_1 deposited under accession number ATCC 98924; or the nucleotide sequence of a mature protein coding sequence of clone yi17_1 deposited under accession number ATCC 98924. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yi17_1 deposited under accession number ATCC 98924. In further preferred embodiments, the

present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:178 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:178, or a polynucleotide encoding a protein comprising a
5 fragment of the amino acid sequence of SEQ ID NO:178 having biological activity, the fragment comprising the amino acid sequence from amino acid 210 to amino acid 219 of SEQ ID NO:178.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:177.

10 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group
15 consisting of:

- (aa) SEQ ID NO:177, but excluding the poly(A) tail at the 3' end of SEQ ID NO:177; and

- (ab) the nucleotide sequence of the cDNA insert of clone
yi17_1 deposited under accession number ATCC 98924;

20 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

- (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- 25 (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- (ba) SEQ ID NO:177, but excluding the poly(A) tail at the
30 3' end of SEQ ID NO:177; and

- (bb) the nucleotide sequence of the cDNA insert of clone
yi17_1 deposited under accession number ATCC 98924;

- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:177, and
5 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:177 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:177, but excluding the poly(A) tail at the 3' end of SEQ ID NO:177. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:177 from nucleotide 85 to nucleotide
10 1377, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:177 from nucleotide 85 to nucleotide 1377, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:177 from nucleotide 85 to nucleotide 1377. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID
15 NO:177 from nucleotide 139 to nucleotide 1377, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:177 from nucleotide 139 to nucleotide 1377, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:177 from nucleotide 139 to nucleotide 1377.

In other embodiments, the present invention provides a composition comprising
20 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:178;
- (b) a fragment of the amino acid sequence of SEQ ID NO:178, the fragment comprising eight contiguous amino acids of SEQ ID NO:178; and
- 25 (c) the amino acid sequence encoded by the cDNA insert of clone yi17_1 deposited under accession number ATCC 98924;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:178. In further preferred embodiments, the present invention provides a protein comprising a fragment of the
30 amino acid sequence of SEQ ID NO:178 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:178, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:178 having biological activity, the fragment comprising the amino acid sequence from amino acid 210 to amino acid 219 of SEQ ID NO:178.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:179;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:179 from nucleotide 50 to nucleotide 1075;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:179 from nucleotide 215 to nucleotide 1075;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yk38_1 deposited under accession number
10 ATCC 98924;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yk38_1 deposited under accession number ATCC 98924;
- (f) a polynucleotide comprising the nucleotide sequence of a mature
15 protein coding sequence of clone yk38_1 deposited under accession number ATCC 98924;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yk38_1 deposited under accession number ATCC 98924;
- (h) a polynucleotide encoding a protein comprising the amino acid
20 sequence of SEQ ID NO:180;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:180 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:180;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of
25 (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 30 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:179.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:179 from nucleotide 50 to nucleotide 1075; the nucleotide sequence of SEQ ID NO:179

from nucleotide 215 to nucleotide 1075; the nucleotide sequence of the full-length protein coding sequence of clone yk38_1 deposited under accession number ATCC 98924; or the nucleotide sequence of a mature protein coding sequence of clone yk38_1 deposited under accession number ATCC 98924. In other preferred embodiments, the polynucleotide
5 encodes the full-length or a mature protein encoded by the cDNA insert of clone yk38_1 deposited under accession number ATCC 98924. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:180 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous
10 amino acids of SEQ ID NO:180, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:180 having biological activity, the fragment comprising the amino acid sequence from amino acid 166 to amino acid 175 of SEQ ID NO:180.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ
15 ID NO:179.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize
20 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:179, but excluding the poly(A) tail at the 3' end of SEQ ID NO:179; and
 - (ab) the nucleotide sequence of the cDNA insert of clone
25 yk38_1 deposited under accession number ATCC 98924;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);
- 30 and
- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:179, but excluding the poly(A) tail at the 3' end of SEQ ID NO:179; and

(bb) the nucleotide sequence of the cDNA insert of clone yk38_1 deposited under accession number ATCC 98924;

5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

10 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:179, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:179 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:179, but excluding the poly(A) tail at the 3' end of SEQ ID NO:179. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence
15 corresponding to the cDNA sequence of SEQ ID NO:179 from nucleotide 50 to nucleotide 1075, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:179 from nucleotide 50 to nucleotide 1075, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:179 from nucleotide 50 to nucleotide 1075. Also preferably the polynucleotide isolated according to the above
20 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:179 from nucleotide 215 to nucleotide 1075, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:179 from nucleotide 215 to nucleotide 1075, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:179 from nucleotide 215 to nucleotide 1075.

25 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:180;

(b) a fragment of the amino acid sequence of SEQ ID NO:180, the
30 fragment comprising eight contiguous amino acids of SEQ ID NO:180; and

(c) the amino acid sequence encoded by the cDNA insert of clone yk38_1 deposited under accession number ATCC 98924;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:180. In further preferred

embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:180 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:180, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:180 having biological activity, the fragment comprising the amino acid sequence from amino acid 166 to amino acid 175 of SEQ ID NO:180.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 10 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:181;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:181 from nucleotide 76 to nucleotide 348;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:181 from nucleotide 139 to nucleotide 348;
- 15 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yk51_1 deposited under accession number ATCC 98924;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yk51_1 deposited under accession number ATCC 98924;
- 20 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yk51_1 deposited under accession number ATCC 98924;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yk51_1 deposited under accession number ATCC 98924;
- 25 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:182;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:182 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:182;
- 30 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:181.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:181 from nucleotide 76 to nucleotide 348; the nucleotide sequence of SEQ ID NO:181 from nucleotide 139 to nucleotide 348; the nucleotide sequence of the full-length protein coding sequence of clone yk51_1 deposited under accession number ATCC 98924; or the nucleotide sequence of a mature protein coding sequence of clone yk51_1 deposited under accession number ATCC 98924. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yk51_1 deposited under accession number ATCC 98924. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:182 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:182, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:182 having biological activity, the fragment comprising the amino acid sequence from amino acid 40 to amino acid 49 of SEQ ID NO:182.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:181.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (aa) SEQ ID NO:181, but excluding the poly(A) tail at the 3' end of SEQ ID NO:181; and
- (ab) the nucleotide sequence of the cDNA insert of clone yk51_1 deposited under accession number ATCC 98924;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

5 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:181, but excluding the poly(A) tail at the 3' end of SEQ ID NO:181; and

10 (bb) the nucleotide sequence of the cDNA insert of clone yk51_1 deposited under accession number ATCC 98924;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

15 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:181, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:181 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:181, but
20 excluding the poly(A) tail at the 3' end of SEQ ID NO:181. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:181 from nucleotide 76 to nucleotide 348, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:181 from nucleotide 76 to nucleotide 348, to a nucleotide
25 sequence corresponding to the 3' end of said sequence of SEQ ID NO:181 from nucleotide 76 to nucleotide 348. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:181 from nucleotide 139 to nucleotide 348, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:181 from
30 nucleotide 139 to nucleotide 348, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:181 from nucleotide 139 to nucleotide 348.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:182;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:182, the fragment comprising eight contiguous amino acids of SEQ ID NO:182; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone yk51_1 deposited under accession number ATCC 98924;
- 5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:182. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:182 having biological activity, the fragment preferably
- 10 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:182, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:182 having biological activity, the fragment comprising the amino acid sequence from amino acid 40 to amino acid 49 of SEQ ID NO:182.

In one embodiment, the present invention provides a composition comprising an

15 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:183;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:183 from nucleotide 203 to nucleotide 577;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yk74_1 deposited under accession number ATCC 98924;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yk74_1 deposited under accession number ATCC 98924;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yk74_1 deposited under accession number ATCC 98924;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yk74_1 deposited under accession number ATCC 98924;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:184;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:184 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:184;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

5 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:183.

10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:183 from nucleotide 203 to nucleotide 577; the nucleotide sequence of the full-length protein coding sequence of clone yk74_1 deposited under accession number ATCC 98924; or the nucleotide sequence of a mature protein coding sequence of clone yk74_1 deposited under accession number ATCC 98924. In other preferred embodiments, the
15 polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yk74_1 deposited under accession number ATCC 98924. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:184 having biological activity, the fragment preferably comprising eight (more preferably twenty, most
20 preferably thirty) contiguous amino acids of SEQ ID NO:184, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:184 having biological activity, the fragment comprising the amino acid sequence from amino acid 57 to amino acid 66 of SEQ ID NO:184.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ
25 ID NO:183.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

30 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:183, but excluding the poly(A) tail at the 3' end of SEQ ID NO:183; and

- (ab) the nucleotide sequence of the cDNA insert of clone yk74_1 deposited under accession number ATCC 98924;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 5 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 10 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:183, but excluding the poly(A) tail at the 3' end of SEQ ID NO:183; and
- (bb) the nucleotide sequence of the cDNA insert of clone yk74_1 deposited under accession number ATCC 98924;
- 15 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- 20 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:183, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:183 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:183, but excluding the poly(A) tail at the 3' end of SEQ ID NO:183. Also preferably the
- 25 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:183 from nucleotide 203 to nucleotide 577, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:183 from nucleotide 203 to nucleotide 577, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:183 from nucleotide
- 30 203 to nucleotide 577.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:184;

- (b) a fragment of the amino acid sequence of SEQ ID NO:184, the fragment comprising eight contiguous amino acids of SEQ ID NO:184; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yk74_1 deposited under accession number ATCC 98924;
- 5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:184. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:184 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 10 of SEQ ID NO:184, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:184 having biological activity, the fragment comprising the amino acid sequence from amino acid 57 to amino acid 66 of SEQ ID NO:184.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:185;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:185 from nucleotide 38 to nucleotide 2170;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yk89_1 deposited under accession number
- 20 ATCC 98924;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yk89_1 deposited under accession number ATCC 98924;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yk89_1 deposited under accession number ATCC
- 25 98924;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yk89_1 deposited under accession number ATCC 98924;
- (g) a polynucleotide encoding a protein comprising the amino acid
- 30 sequence of SEQ ID NO:186;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:186 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:186;

- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
 - (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
 - 5 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
 - (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:185.
- 10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:185 from nucleotide 38 to nucleotide 2170; the nucleotide sequence of the full-length protein coding sequence of clone yk89_1 deposited under accession number ATCC 98924; or the nucleotide sequence of a mature protein coding sequence of clone yk89_1 deposited under accession number ATCC 98924. In other preferred embodiments, the
- 15 polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yk89_1 deposited under accession number ATCC 98924. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:186 having biological activity, the fragment preferably comprising eight (more preferably twenty, most
- 20 preferably thirty) contiguous amino acids of SEQ ID NO:186, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:186 having biological activity, the fragment comprising the amino acid sequence from amino acid 350 to amino acid 359 of SEQ ID NO:186.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:185.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize
 - 30 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:185, but excluding the poly(A) tail at the 3' end of SEQ ID NO:185; and

- (ab) the nucleotide sequence of the cDNA insert of clone yk89_1 deposited under accession number ATCC 98924;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 5 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 10 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:185, but excluding the poly(A) tail at the 3' end of SEQ ID NO:185; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 15 yk89_1 deposited under accession number ATCC 98924;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- 20 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:185, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:185 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:185, but excluding the poly(A) tail at the 3' end of SEQ ID NO:185. Also preferably the
- 25 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:185 from nucleotide 38 to nucleotide 2170, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:185 from nucleotide 38 to nucleotide 2170, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:185 from nucleotide
- 30 38 to nucleotide 2170.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:186;

- (b) a fragment of the amino acid sequence of SEQ ID NO:186, the fragment comprising eight contiguous amino acids of SEQ ID NO:186; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yk89_1 deposited under accession number ATCC 98924;
- 5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:186. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:186 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 10 of SEQ ID NO:186, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:186 having biological activity, the fragment comprising the amino acid sequence from amino acid 350 to amino acid 359 of SEQ ID NO:186.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:187;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:187 from nucleotide 14 to nucleotide 742;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
- 20 NO:187 from nucleotide 89 to nucleotide 742;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone y118_1 deposited under accession number ATCC 98924;
- (e) a polynucleotide encoding the full-length protein encoded by the
- 25 cDNA insert of clone y118_1 deposited under accession number ATCC 98924;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone y118_1 deposited under accession number ATCC 98924;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA
- 30 insert of clone y118_1 deposited under accession number ATCC 98924;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:188;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:188 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:188;

5 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

10 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:187.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:187 from nucleotide 14 to nucleotide 742; the nucleotide sequence of SEQ ID NO:187
15 from nucleotide 89 to nucleotide 742; the nucleotide sequence of the full-length protein coding sequence of clone yl18_1 deposited under accession number ATCC 98924; or the nucleotide sequence of a mature protein coding sequence of clone yl18_1 deposited under accession number ATCC 98924. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yl18_1
20 deposited under accession number ATCC 98924. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:188 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:188, or a polynucleotide encoding a protein comprising a
25 fragment of the amino acid sequence of SEQ ID NO:188 having biological activity, the fragment comprising the amino acid sequence from amino acid 116 to amino acid 125 of SEQ ID NO:188.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:187.

30 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:187, but excluding the poly(A) tail at the 3' end of SEQ ID NO:187; and

(ab) the nucleotide sequence of the cDNA insert of clone yl18_1 deposited under accession number ATCC 98924;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:187, but excluding the poly(A) tail at the 3' end of SEQ ID NO:187; and

(bb) the nucleotide sequence of the cDNA insert of clone yl18_1 deposited under accession number ATCC 98924;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:187, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:187 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:187, but excluding the poly(A) tail at the 3' end of SEQ ID NO:187. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:187 from nucleotide 14 to nucleotide 742, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:187 from nucleotide 14 to nucleotide 742, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:187 from nucleotide

14 to nucleotide 742. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:187 from nucleotide 89 to nucleotide 742, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:187 from
5 nucleotide 89 to nucleotide 742, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:187 from nucleotide 89 to nucleotide 742.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:188;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:188, the fragment comprising eight contiguous amino acids of SEQ ID NO:188; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone y118_1 deposited under accession number ATCC 98924;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:188. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:188 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
20 of SEQ ID NO:188, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:188 having biological activity, the fragment comprising the amino acid sequence from amino acid 116 to amino acid 125 of SEQ ID NO:188.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:189;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:189 from nucleotide 280 to nucleotide 615;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
30 NO:189 from nucleotide 325 to nucleotide 615;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yb325_1 deposited under accession number ATCC 98958;

- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yb325_1 deposited under accession number ATCC 98958;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yb325_1 deposited under accession number ATCC 98958;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yb325_1 deposited under accession number ATCC 98958;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:190;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:190 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:190;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:189.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:189 from nucleotide 280 to nucleotide 615; the nucleotide sequence of SEQ ID NO:189 from nucleotide 325 to nucleotide 615; the nucleotide sequence of the full-length protein coding sequence of clone yb325_1 deposited under accession number ATCC 98958; or the nucleotide sequence of a mature protein coding sequence of clone yb325_1 deposited under accession number ATCC 98958. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yb325_1 deposited under accession number ATCC 98958. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:190 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:190, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:190

having biological activity, the fragment comprising the amino acid sequence from amino acid 51 to amino acid 60 of SEQ ID NO:190.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:189.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize
10 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:189; and

(ab) the nucleotide sequence of the cDNA insert of clone
yb325_1 deposited under accession number ATCC 98958;

(ii) hybridizing said probe(s) to human genomic DNA in
15 conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the
probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that
20 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:189; and

(bb) the nucleotide sequence of the cDNA insert of clone
25 yb325_1 deposited under accession number ATCC 98958;

(ii) hybridizing said primer(s) to human genomic DNA in
conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

30 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:189, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:189 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:189. Also preferably the polynucleotide isolated according to the above process comprises a

nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:189 from nucleotide 280 to nucleotide 615, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:189 from nucleotide 280 to nucleotide 615, to a nucleotide sequence corresponding to the 3' end of said sequence of
5 SEQ ID NO:189 from nucleotide 280 to nucleotide 615. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:189 from nucleotide 325 to nucleotide 615, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:189 from nucleotide 325 to nucleotide 615, to a nucleotide
10 sequence corresponding to the 3' end of said sequence of SEQ ID NO:189 from nucleotide 325 to nucleotide 615.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 15 (a) the amino acid sequence of SEQ ID NO:190;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:190, the fragment comprising eight contiguous amino acids of SEQ ID NO:190; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone yb325_1 deposited under accession number ATCC 98958;
- 20 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:190. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:190 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
25 of SEQ ID NO:190, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:190 having biological activity, the fragment comprising the amino acid sequence from amino acid 51 to amino acid 60 of SEQ ID NO:190.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 30 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:191;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:191 from nucleotide 163 to nucleotide 429;

- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:191 from nucleotide 274 to nucleotide 429;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yd261_1 deposited under accession number ATCC 98958;
- 5 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yd261_1 deposited under accession number ATCC 98958;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yd261_1 deposited under accession number ATCC 98958;
- 10 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yd261_1 deposited under accession number ATCC 98958;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:192;
- 15 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:192 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:192;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- 20 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:191.
- 25

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:191 from nucleotide 163 to nucleotide 429; the nucleotide sequence of SEQ ID NO:191 from nucleotide 274 to nucleotide 429; the nucleotide sequence of the full-length protein coding sequence of clone yd261_1 deposited under accession number ATCC 98958; or the nucleotide sequence of a mature protein coding sequence of clone yd261_1 deposited under accession number ATCC 98958. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yd261_1 deposited under accession number ATCC 98958. In further preferred

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embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:192 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:192, or a polynucleotide
5 encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:192 having biological activity, the fragment comprising the amino acid sequence from amino acid 39 to amino acid 48 of SEQ ID NO:192.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:191.

10 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group
15 consisting of:

(aa) SEQ ID NO:191, but excluding the poly(A) tail at the 3' end of SEQ ID NO:191; and

(ab) the nucleotide sequence of the cDNA insert of clone yd261_1 deposited under accession number ATCC 98958;

20 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

25 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

30 (ba) SEQ ID NO:191, but excluding the poly(A) tail at the 3' end of SEQ ID NO:191; and

(bb) the nucleotide sequence of the cDNA insert of clone yd261_1 deposited under accession number ATCC 98958;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:191, and
5 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:191 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:191, but excluding the poly(A) tail at the 3' end of SEQ ID NO:191. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:191 from nucleotide 163 to nucleotide
10 429, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:191 from nucleotide 163 to nucleotide 429, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:191 from nucleotide 163 to nucleotide 429. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID
15 NO:191 from nucleotide 274 to nucleotide 429, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:191 from nucleotide 274 to nucleotide 429, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:191 from nucleotide 274 to nucleotide 429.

In other embodiments, the present invention provides a composition comprising
20 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:192;
- (b) a fragment of the amino acid sequence of SEQ ID NO:192, the fragment comprising eight contiguous amino acids of SEQ ID NO:192; and
- 25 (c) the amino acid sequence encoded by the cDNA insert of clone yd261_1 deposited under accession number ATCC 98958;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:192. In further preferred embodiments, the present invention provides a protein comprising a fragment of the
30 amino acid sequence of SEQ ID NO:192 having biological activity, the fragment preferably

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:193;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:193 from nucleotide 1262 to nucleotide 1858;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yh33_1 deposited under accession number ATCC 98958;
- 10 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yh33_1 deposited under accession number ATCC 98958;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yh33_1 deposited under accession number ATCC 98958;
- 15 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yh33_1 deposited under accession number ATCC 98958;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:194;
- (h) a polynucleotide encoding a protein comprising a fragment of the
20 amino acid sequence of SEQ ID NO:194 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:194;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein
25 of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any
30 one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:193.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:193 from nucleotide 1262 to nucleotide 1858; the nucleotide sequence of the full-length protein coding sequence of clone yh33_1 deposited under accession number ATCC 98958; or the nucleotide sequence of a mature protein coding sequence of clone yh33_1

deposited under accession number ATCC 98958. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yh33_1 deposited under accession number ATCC 98958. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:194 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:194, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:194 having biological activity, the fragment comprising the amino acid sequence from amino acid 94 to amino acid 103 of SEQ ID NO:194.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:193.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 15 (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - 20 (aa) SEQ ID NO:193, but excluding the poly(A) tail at the 3' end of SEQ ID NO:193; and
 - (ab) the nucleotide sequence of the cDNA insert of clone yh33_1 deposited under accession number ATCC 98958;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - 25 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
 - 30 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (ba) SEQ ID NO:193, but excluding the poly(A) tail at the 3' end of SEQ ID NO:193; and

(bb) the nucleotide sequence of the cDNA insert of clone yh33_1 deposited under accession number ATCC 98958;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

5 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:193, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ
10 ID NO:193 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:193, but excluding the poly(A) tail at the 3' end of SEQ ID NO:193. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:193 from nucleotide 1262 to nucleotide 1858, and extending contiguously from a nucleotide sequence corresponding
15 to the 5' end of said sequence of SEQ ID NO:193 from nucleotide 1262 to nucleotide 1858, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:193 from nucleotide 1262 to nucleotide 1858.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group
20 consisting of:

(a) the amino acid sequence of SEQ ID NO:194;

(b) a fragment of the amino acid sequence of SEQ ID NO:194, the fragment comprising eight contiguous amino acids of SEQ ID NO:194; and

(c) the amino acid sequence encoded by the cDNA insert of clone
25 yh33_1 deposited under accession number ATCC 98958;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:194. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:194 having biological activity, the fragment preferably
30 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:194, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:194 having biological activity, the fragment comprising the amino acid sequence from amino acid 94 to amino acid 103 of SEQ ID NO:194.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:195;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:195 from nucleotide 25 to nucleotide 1851;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:195 from nucleotide 250 to nucleotide 1851;
- 10 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yi16_1 deposited under accession number ATCC 98958;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yi16_1 deposited under accession number ATCC 98958;
- 15 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yi16_1 deposited under accession number ATCC 98958;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yi16_1 deposited under accession number ATCC 98958;
- 20 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:196;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:196 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:196;
- 25 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 30 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:195.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:195 from nucleotide 25 to nucleotide 1851; the nucleotide sequence of SEQ ID NO:195

from nucleotide 250 to nucleotide 1851; the nucleotide sequence of the full-length protein coding sequence of clone yi16_1 deposited under accession number ATCC 98958; or the nucleotide sequence of a mature protein coding sequence of clone yi16_1 deposited under accession number ATCC 98958. In other preferred embodiments, the polynucleotide
5 encodes the full-length or a mature protein encoded by the cDNA insert of clone yi16_1 deposited under accession number ATCC 98958. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:196 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous
10 amino acids of SEQ ID NO:196, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:196 having biological activity, the fragment comprising the amino acid sequence from amino acid 299 to amino acid 308 of SEQ ID NO:196.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ
15 ID NO:195.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize
20 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:195, but excluding the poly(A) tail at the 3' end of SEQ ID NO:195; and
 - (ab) the nucleotide sequence of the cDNA insert of clone
25 yi16_1 deposited under accession number ATCC 98958;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);
30
- and
- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:195, but excluding the poly(A) tail at the 3' end of SEQ ID NO:195; and

(bb) the nucleotide sequence of the cDNA insert of clone yi16_1 deposited under accession number ATCC 98958;

5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a
10 nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:195, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:195 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:195, but excluding the poly(A) tail at the 3' end of SEQ ID NO:195. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence
15 corresponding to the cDNA sequence of SEQ ID NO:195 from nucleotide 25 to nucleotide 1851, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:195 from nucleotide 25 to nucleotide 1851, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:195 from nucleotide 25 to nucleotide 1851. Also preferably the polynucleotide isolated according to the above
20 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:195 from nucleotide 250 to nucleotide 1851, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:195 from nucleotide 250 to nucleotide 1851, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:195 from nucleotide 250 to nucleotide 1851.

25 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:196;

(b) a fragment of the amino acid sequence of SEQ ID NO:196, the
30 fragment comprising eight contiguous amino acids of SEQ ID NO:196; and

(c) the amino acid sequence encoded by the cDNA insert of clone yi16_1 deposited under accession number ATCC 98958;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:196. In further preferred

embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:196 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:196, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:196 having biological activity, the fragment comprising the amino acid sequence from amino acid 299 to amino acid 308 of SEQ ID NO:196.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 10 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:197;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:197 from nucleotide 739 to nucleotide 996;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yk46_1 deposited under accession number ATCC 98958;
- 15 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yk46_1 deposited under accession number ATCC 98958;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yk46_1 deposited under accession number ATCC 98958;
- 20 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yk46_1 deposited under accession number ATCC 98958;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:198;
- 25 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:198 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:198;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- 30 (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:197.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:197 from nucleotide 739 to nucleotide 996; the nucleotide sequence of the full-length protein coding sequence of clone yk46_1 deposited under accession number ATCC 98958; or the nucleotide sequence of a mature protein coding sequence of clone yk46_1 deposited under accession number ATCC 98958. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yk46_1 deposited under accession number ATCC 98958. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:198 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:198, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:198 having biological activity, the fragment comprising the amino acid sequence from amino acid 38 to amino acid 47 of SEQ ID NO:198.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:197.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:197, but excluding the poly(A) tail at the 3' end of SEQ ID NO:197; and
 - (ab) the nucleotide sequence of the cDNA insert of clone yk46_1 deposited under accession number ATCC 98958;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (ba) SEQ ID NO:197, but excluding the poly(A) tail at the 3' end of SEQ ID NO:197; and

(bb) the nucleotide sequence of the cDNA insert of clone yk46_1 deposited under accession number ATCC 98958;

10 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:197, and
15 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:197 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:197, but excluding the poly(A) tail at the 3' end of SEQ ID NO:197. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:197 from nucleotide 739 to nucleotide
20 996, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:197 from nucleotide 739 to nucleotide 996, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:197 from nucleotide 739 to nucleotide 996.

In other embodiments, the present invention provides a composition comprising
25 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:198;

(b) a fragment of the amino acid sequence of SEQ ID NO:198, the fragment comprising eight contiguous amino acids of SEQ ID NO:198; and

30 (c) the amino acid sequence encoded by the cDNA insert of clone yk46_1 deposited under accession number ATCC 98958;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:198. In further preferred embodiments, the present invention provides a protein comprising a fragment of the

amino acid sequence of SEQ ID NO:198 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:198, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:198 having biological activity, the fragment comprising the amino acid sequence
5 from amino acid 38 to amino acid 47 of SEQ ID NO:198.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:199;
- 10 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:199 from nucleotide 222 to nucleotide 605;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:199 from nucleotide 366 to nucleotide 605;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yk84_1 deposited under accession number
15 ATCC 98958;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yk84_1 deposited under accession number ATCC 98958;
- (f) a polynucleotide comprising the nucleotide sequence of a mature
20 protein coding sequence of clone yk84_1 deposited under accession number ATCC 98958;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yk84_1 deposited under accession number ATCC 98958;
- (h) a polynucleotide encoding a protein comprising the amino acid
25 sequence of SEQ ID NO:200;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:200 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:200;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of
30 (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:199.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:199 from nucleotide 222 to nucleotide 605; the nucleotide sequence of SEQ ID NO:199 from nucleotide 366 to nucleotide 605; the nucleotide sequence of the full-length protein coding sequence of clone yk84_1 deposited under accession number ATCC 98958; or the nucleotide sequence of a mature protein coding sequence of clone yk84_1 deposited under accession number ATCC 98958. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yk84_1 deposited under accession number ATCC 98958. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:200 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:200, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:200 having biological activity, the fragment comprising the amino acid sequence from amino acid 59 to amino acid 68 of SEQ ID NO:200.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:199.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:199, but excluding the poly(A) tail at the 3' end of SEQ ID NO:199; and
 - (ab) the nucleotide sequence of the cDNA insert of clone yk84_1 deposited under accession number ATCC 98958;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:199, but excluding the poly(A) tail at the 3' end of SEQ ID NO:199; and

(bb) the nucleotide sequence of the cDNA insert of clone yk84_1 deposited under accession number ATCC 98958;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:199, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:199 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:199, but excluding the poly(A) tail at the 3' end of SEQ ID NO:199. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:199 from nucleotide 222 to nucleotide 605, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:199 from nucleotide 222 to nucleotide 605, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:199 from nucleotide 222 to nucleotide 605. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:199 from nucleotide 366 to nucleotide 605, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:199 from nucleotide 366 to nucleotide 605, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:199 from nucleotide 366 to nucleotide 605.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:200;

- (b) a fragment of the amino acid sequence of SEQ ID NO:200, the fragment comprising eight contiguous amino acids of SEQ ID NO:200; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yk84_1 deposited under accession number ATCC 98958;
- 5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:200. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:200 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 10 of SEQ ID NO:200, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:200 having biological activity, the fragment comprising the amino acid sequence from amino acid 59 to amino acid 68 of SEQ ID NO:200.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:201;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:201 from nucleotide 140 to nucleotide 1036;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
- 20 NO:201 from nucleotide 269 to nucleotide 1036;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yk143_1 deposited under accession number ATCC 98958;
- (e) a polynucleotide encoding the full-length protein encoded by the
- 25 cDNA insert of clone yk143_1 deposited under accession number ATCC 98958;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yk143_1 deposited under accession number ATCC 98958;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA
- 30 insert of clone yk143_1 deposited under accession number ATCC 98958;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:202;

- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:202 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:202;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:201.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:201 from nucleotide 140 to nucleotide 1036; the nucleotide sequence of SEQ ID NO:201 from nucleotide 269 to nucleotide 1036; the nucleotide sequence of the full-length protein coding sequence of clone yk143_1 deposited under accession number ATCC 98958; or the nucleotide sequence of a mature protein coding sequence of clone yk143_1 deposited under accession number ATCC 98958. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yk143_1 deposited under accession number ATCC 98958. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:202 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:202, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:202 having biological activity, the fragment comprising the amino acid sequence from amino acid 144 to amino acid 153 of SEQ ID NO:202.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:201.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:201, but excluding the poly(A) tail at the 3' end of SEQ ID NO:201; and

(ab) the nucleotide sequence of the cDNA insert of clone yk143_1 deposited under accession number ATCC 98958;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:201, but excluding the poly(A) tail at the 3' end of SEQ ID NO:201; and

(bb) the nucleotide sequence of the cDNA insert of clone yk143_1 deposited under accession number ATCC 98958;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:201, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:201 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:201, but excluding the poly(A) tail at the 3' end of SEQ ID NO:201. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:201 from nucleotide 140 to nucleotide 1036, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:201 from nucleotide 140 to nucleotide 1036, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:201 from nucleotide

140 to nucleotide 1036. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:201 from nucleotide 269 to nucleotide 1036, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:201 from
5 nucleotide 269 to nucleotide 1036, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:201 from nucleotide 269 to nucleotide 1036.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:202;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:202, the fragment comprising eight contiguous amino acids of SEQ ID NO:202; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone yk143_1 deposited under accession number ATCC 98958;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:202. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:202 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
20 of SEQ ID NO:202, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:202 having biological activity, the fragment comprising the amino acid sequence from amino acid 144 to amino acid 153 of SEQ ID NO:202.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:203;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:203 from nucleotide 304 to nucleotide 636;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
30 NO:203 from nucleotide 415 to nucleotide 636;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yk156_1 deposited under accession number ATCC 98958;

- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yk156_1 deposited under accession number ATCC 98958;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yk156_1 deposited under accession number ATCC 98958;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yk156_1 deposited under accession number ATCC 98958;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:204;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:204 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:204;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:203.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:203 from nucleotide 304 to nucleotide 636; the nucleotide sequence of SEQ ID NO:203 from nucleotide 415 to nucleotide 636; the nucleotide sequence of the full-length protein coding sequence of clone yk156_1 deposited under accession number ATCC 98958; or the nucleotide sequence of a mature protein coding sequence of clone yk156_1 deposited under accession number ATCC 98958. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yk156_1 deposited under accession number ATCC 98958. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:204 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:204, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:204

having biological activity, the fragment comprising the amino acid sequence from amino acid 50 to amino acid 59 of SEQ ID NO:204.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:203.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize
10 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:203, but excluding the poly(A) tail at the
3' end of SEQ ID NO:203; and

(ab) the nucleotide sequence of the cDNA insert of clone
yk156_1 deposited under accession number ATCC 98958;

15 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the
probe(s);

and

20 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that
hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from
the group consisting of:

(ba) SEQ ID NO:203, but excluding the poly(A) tail at the
25 3' end of SEQ ID NO:203; and

(bb) the nucleotide sequence of the cDNA insert of clone
yk156_1 deposited under accession number ATCC 98958;

(ii) hybridizing said primer(s) to human genomic DNA in
conditions at least as stringent as 4X SSC at 50 degrees C;

30 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:203, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

ID NO:203 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:203, but excluding the poly(A) tail at the 3' end of SEQ ID NO:203. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:203 from nucleotide 304 to nucleotide 636, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:203 from nucleotide 304 to nucleotide 636, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:203 from nucleotide 304 to nucleotide 636. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:203 from nucleotide 415 to nucleotide 636, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:203 from nucleotide 415 to nucleotide 636, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:203 from nucleotide 415 to nucleotide 636.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:204;
- (b) a fragment of the amino acid sequence of SEQ ID NO:204, the fragment comprising eight contiguous amino acids of SEQ ID NO:204; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yk156_1 deposited under accession number ATCC 98958;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:204. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:204 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:204, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:204 having biological activity, the fragment comprising the amino acid sequence from amino acid 50 to amino acid 59 of SEQ ID NO:204.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:205;

- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:205 from nucleotide 571 to nucleotide 891;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:205 from nucleotide 745 to nucleotide 891;
- 5 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yk204_1 deposited under accession number ATCC 98958;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yk204_1 deposited under accession number ATCC 98958;
- 10 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yk204_1 deposited under accession number ATCC 98958;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yk204_1 deposited under accession number ATCC 98958;
- 15 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:206;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:206 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:206;
- 20 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 25 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:205.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:205 from nucleotide 571 to nucleotide 891; the nucleotide sequence of SEQ ID NO:205 from nucleotide 745 to nucleotide 891; the nucleotide sequence of the full-length protein coding sequence of clone yk204_1 deposited under accession number ATCC 98958; or the nucleotide sequence of a mature protein coding sequence of clone yk204_1 deposited under accession number ATCC 98958. In other preferred embodiments, the

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polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yk204_1 deposited under accession number ATCC 98958. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:206 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:206, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:206 having biological activity, the fragment comprising the amino acid sequence from amino acid 48 to amino acid 57 of SEQ ID NO:206.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:205.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:
(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:205, but excluding the poly(A) tail at the 3' end of SEQ ID NO:205; and

(ab) the nucleotide sequence of the cDNA insert of clone yk204_1 deposited under accession number ATCC 98958;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:
(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:205, but excluding the poly(A) tail at the 3' end of SEQ ID NO:205; and

(bb) the nucleotide sequence of the cDNA insert of clone yk204_1 deposited under accession number ATCC 98958;

- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

5 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:205, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:205 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:205, but excluding the poly(A) tail at the 3' end of SEQ ID NO:205. Also preferably the
10 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:205 from nucleotide 571 to nucleotide 891, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:205 from nucleotide 571 to nucleotide 891, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:205 from nucleotide
15 571 to nucleotide 891. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:205 from nucleotide 745 to nucleotide 891, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:205 from nucleotide 745 to nucleotide 891, to a nucleotide sequence corresponding to the 3' end of
20 said sequence of SEQ ID NO:205 from nucleotide 745 to nucleotide 891.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:206;
- 25 (b) a fragment of the amino acid sequence of SEQ ID NO:206, the fragment comprising eight contiguous amino acids of SEQ ID NO:206; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yk204_1 deposited under accession number ATCC 98958;

the protein being substantially free from other mammalian proteins. Preferably such
30 protein comprises the amino acid sequence of SEQ ID NO:206. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:206 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:206, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:206 having biological activity, the fragment comprising the amino acid sequence from amino acid 48 to amino acid 57 of SEQ ID NO:206.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:207;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:207 from nucleotide 283 to nucleotide 1560;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yk224_1 deposited under accession
10 number ATCC 98958;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yk224_1 deposited under accession number ATCC 98958;
- (e) a polynucleotide comprising the nucleotide sequence of a mature
15 protein coding sequence of clone yk224_1 deposited under accession number ATCC 98958;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yk224_1 deposited under accession number ATCC 98958;
- (g) a polynucleotide encoding a protein comprising the amino acid
20 sequence of SEQ ID NO:208;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:208 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:208;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of
25 (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:207.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:207 from nucleotide 283 to nucleotide 1560; the nucleotide sequence of the full-length

protein coding sequence of clone yk224_1 deposited under accession number ATCC 98958; or the nucleotide sequence of a mature protein coding sequence of clone yk224_1 deposited under accession number ATCC 98958. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yk224_1 deposited under accession number ATCC 98958. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:208 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:208, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:208 having biological activity, the fragment comprising the amino acid sequence from amino acid 208 to amino acid 217 of SEQ ID NO:208.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:207.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:207, but excluding the poly(A) tail at the 3' end of SEQ ID NO:207; and

(ab) the nucleotide sequence of the cDNA insert of clone yk224_1 deposited under accession number ATCC 98958;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:207, but excluding the poly(A) tail at the 3' end of SEQ ID NO:207; and

(bb) the nucleotide sequence of the cDNA insert of clone yk224_1 deposited under accession number ATCC 98958;

5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

10 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:207, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:207 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:207, but excluding the poly(A) tail at the 3' end of SEQ ID NO:207. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence
15 corresponding to the cDNA sequence of SEQ ID NO:207 from nucleotide 283 to nucleotide 1560, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:207 from nucleotide 283 to nucleotide 1560, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:207 from nucleotide 283 to nucleotide 1560.

20 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:208;

25 (b) a fragment of the amino acid sequence of SEQ ID NO:208, the fragment comprising eight contiguous amino acids of SEQ ID NO:208; and

(c) the amino acid sequence encoded by the cDNA insert of clone yk224_1 deposited under accession number ATCC 98958;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:208. In further preferred
30 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:208 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:208, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:208 having biological activity, the fragment comprising the amino acid sequence from amino acid 208 to amino acid 217 of SEQ ID NO:208.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:209;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:209 from nucleotide 485 to nucleotide 1465;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
10 NO:209 from nucleotide 560 to nucleotide 1465;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yk261_1 deposited under accession number ATCC 98958;
- (e) a polynucleotide encoding the full-length protein encoded by the
15 cDNA insert of clone yk261_1 deposited under accession number ATCC 98958;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yk261_1 deposited under accession number ATCC 98958;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA
20 insert of clone yk261_1 deposited under accession number ATCC 98958;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:210;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:210 having biological activity, the fragment
25 comprising eight contiguous amino acids of SEQ ID NO:210;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:209.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:209 from nucleotide 485 to nucleotide 1465; the nucleotide sequence of SEQ ID NO:209 from nucleotide 560 to nucleotide 1465; the nucleotide sequence of the full-length protein coding sequence of clone yk261_1 deposited under accession number ATCC 98958; or the nucleotide sequence of a mature protein coding sequence of clone yk261_1 deposited under accession number ATCC 98958. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yk261_1 deposited under accession number ATCC 98958. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:210 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:210, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:210 having biological activity, the fragment comprising the amino acid sequence from amino acid 158 to amino acid 167 of SEQ ID NO:210.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:209.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 20 (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - 25 (aa) SEQ ID NO:209, but excluding the poly(A) tail at the 3' end of SEQ ID NO:209; and
 - (ab) the nucleotide sequence of the cDNA insert of clone yk261_1 deposited under accession number ATCC 98958;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - 30 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- 5 (ba) SEQ ID NO:209, but excluding the poly(A) tail at the 3' end of SEQ ID NO:209; and
- (bb) the nucleotide sequence of the cDNA insert of clone yk261_1 deposited under accession number ATCC 98958;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 10 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:209, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

15 ID NO:209 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:209, but excluding the poly(A) tail at the 3' end of SEQ ID NO:209. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:209 from nucleotide 485 to nucleotide 1465, and extending contiguously from a nucleotide sequence corresponding to the 5' end

20 of said sequence of SEQ ID NO:209 from nucleotide 485 to nucleotide 1465, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:209 from nucleotide 485 to nucleotide 1465. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:209 from nucleotide 560 to nucleotide 1465, and extending contiguously from a

25 nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:209 from nucleotide 560 to nucleotide 1465, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:209 from nucleotide 560 to nucleotide 1465.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group

30 consisting of:

- (a) the amino acid sequence of SEQ ID NO:210;
- (b) a fragment of the amino acid sequence of SEQ ID NO:210, the fragment comprising eight contiguous amino acids of SEQ ID NO:210; and

(c) the amino acid sequence encoded by the cDNA insert of clone yk261_1 deposited under accession number ATCC 98958; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:210. In further preferred
5 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:210 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:210, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:210 having biological activity, the fragment comprising the amino acid sequence
10 from amino acid 158 to amino acid 167 of SEQ ID NO:210.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:211;
- 15 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:211 from nucleotide 96 to nucleotide 821;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ys3_1 deposited under accession number ATCC 98958;
- 20 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ys3_1 deposited under accession number ATCC 98958;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ys3_1 deposited under accession number ATCC 98958;
- 25 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ys3_1 deposited under accession number ATCC 98958;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:212;
- (h) a polynucleotide encoding a protein comprising a fragment of the
30 amino acid sequence of SEQ ID NO:212 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:212;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

5 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:211.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:211 from nucleotide 96 to nucleotide 821; the nucleotide sequence of the full-length
10 protein coding sequence of clone ys3_1 deposited under accession number ATCC 98958; or the nucleotide sequence of a mature protein coding sequence of clone ys3_1 deposited under accession number ATCC 98958. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ys3_1 deposited under accession number ATCC 98958. In further preferred
15 embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:212 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:212, or a polynucleotide
20 encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:212 having biological activity, the fragment comprising the amino acid sequence from amino acid 116 to amino acid 125 of SEQ ID NO:212.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:211.

Further embodiments of the invention provide isolated polynucleotides produced
25 according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

30 (aa) SEQ ID NO:211, but excluding the poly(A) tail at the 3' end of SEQ ID NO:211; and

(ab) the nucleotide sequence of the cDNA insert of clone ys3_1 deposited under accession number ATCC 98958;

- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- (iii) isolating the DNA polynucleotides detected with the probe(s);
- 5 and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- 10 (ba) SEQ ID NO:211, but excluding the poly(A) tail at the 3' end of SEQ ID NO:211; and
- (bb) the nucleotide sequence of the cDNA insert of clone ys3_1 deposited under accession number ATCC 98958;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 15 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:211, and

20 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:211 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:211, but excluding the poly(A) tail at the 3' end of SEQ ID NO:211. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:211 from nucleotide 96 to nucleotide

25 821, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:211 from nucleotide 96 to nucleotide 821, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:211 from nucleotide 96 to nucleotide 821.

In other embodiments, the present invention provides a composition comprising

30 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:212;
- (b) a fragment of the amino acid sequence of SEQ ID NO:212, the fragment comprising eight contiguous amino acids of SEQ ID NO:212; and

(c) the amino acid sequence encoded by the cDNA insert of clone ys3_1 deposited under accession number ATCC 98958; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:212. In further preferred
5 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:212 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:212, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:212 having biological activity, the fragment comprising the amino acid sequence
10 from amino acid 116 to amino acid 125 of SEQ ID NO:212.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:213;
- 15 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:213 from nucleotide 191 to nucleotide 499;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:213 from nucleotide 317 to nucleotide 499;
- (d) a polynucleotide comprising the nucleotide sequence of the full-
20 length protein coding sequence of clone ys10_1 deposited under accession number ATCC 98958;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ys10_1 deposited under accession number ATCC 98958;
- (f) a polynucleotide comprising the nucleotide sequence of a mature
25 protein coding sequence of clone ys10_1 deposited under accession number ATCC 98958;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ys10_1 deposited under accession number ATCC 98958;
- (h) a polynucleotide encoding a protein comprising the amino acid
30 sequence of SEQ ID NO:214;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:214 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:214;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

5 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:213.

10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:213 from nucleotide 191 to nucleotide 499; the nucleotide sequence of SEQ ID NO:213 from nucleotide 317 to nucleotide 499; the nucleotide sequence of the full-length protein coding sequence of clone ys10_1 deposited under accession number ATCC 98958; or the nucleotide sequence of a mature protein coding sequence of clone ys10_1 deposited under
15 accession number ATCC 98958. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ys10_1 deposited under accession number ATCC 98958. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:214 having biological activity, the fragment
20 preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:214, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:214 having biological activity, the fragment comprising the amino acid sequence from amino acid 46 to amino acid 55 of SEQ ID NO:214.

25 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:213.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:
30 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:213, but excluding the poly(A) tail at the 3' end of SEQ ID NO:213; and

- (ab) the nucleotide sequence of the cDNA insert of clone
ys10_1 deposited under accession number ATCC 98958;
- (ii) hybridizing said probe(s) to human genomic DNA in
conditions at least as stringent as 4X SSC at 50 degrees C; and
- 5 (iii) isolating the DNA polynucleotides detected with the
probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
10 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from
the group consisting of:
- (ba) SEQ ID NO:213, but excluding the poly(A) tail at the
3' end of SEQ ID NO:213; and
- (bb) the nucleotide sequence of the cDNA insert of clone
15 ys10_1 deposited under accession number ATCC 98958;
- (ii) hybridizing said primer(s) to human genomic DNA in
conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- 20 Preferably the polynucleotide isolated according to the above process comprises a
nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:213, and
extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ
ID NO:213 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:213, but
excluding the poly(A) tail at the 3' end of SEQ ID NO:213. Also preferably the
- 25 polynucleotide isolated according to the above process comprises a nucleotide sequence
corresponding to the cDNA sequence of SEQ ID NO:213 from nucleotide 191 to nucleotide
499, and extending contiguously from a nucleotide sequence corresponding to the 5' end
of said sequence of SEQ ID NO:213 from nucleotide 191 to nucleotide 499, to a nucleotide
sequence corresponding to the 3' end of said sequence of SEQ ID NO:213 from nucleotide
- 30 191 to nucleotide 499. Also preferably the polynucleotide isolated according to the above
process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID
NO:213 from nucleotide 317 to nucleotide 499, and extending contiguously from a
nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:213 from

nucleotide 317 to nucleotide 499, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:213 from nucleotide 317 to nucleotide 499.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group
5 consisting of:

- (a) the amino acid sequence of SEQ ID NO:214;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:214, the fragment comprising eight contiguous amino acids of SEQ ID NO:214; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone
10 ys10_1 deposited under accession number ATCC 98958;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:214. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:214 having biological activity, the fragment preferably
15 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:214, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:214 having biological activity, the fragment comprising the amino acid sequence from amino acid 46 to amino acid 55 of SEQ ID NO:214.

In certain preferred embodiments, the polynucleotide is operably linked to an
20 expression control sequence. The invention also provides a host cell, including bacterial, yeast, insect and mammalian cells, transformed with such polynucleotide compositions. Also provided by the present invention are organisms that have enhanced, reduced, or modified expression of the gene(s) corresponding to the polynucleotide sequences disclosed herein.

25 Processes are also provided for producing a protein, which comprise:

- (a) growing a culture of the host cell transformed with such polynucleotide compositions in a suitable culture medium; and
- (b) purifying the protein from the culture.

The protein produced according to such methods is also provided by the present
30 invention.

Protein compositions of the present invention may further comprise a pharmaceutically acceptable carrier. Compositions comprising an antibody which specifically reacts with such protein are also provided by the present invention.

Methods are also provided for preventing, treating or ameliorating a medical condition which comprises administering to a mammalian subject a therapeutically effective amount of a composition comprising a protein of the present invention and a pharmaceutically acceptable carrier.

5

BRIEF DESCRIPTION OF THE DRAWINGS

Figures 1A and 1B are schematic representations of the pED6 and pNOTs vectors, respectively, used for deposit of clones disclosed herein.

10

DETAILED DESCRIPTION

ISOLATED PROTEINS AND POLYNUCLEOTIDES

Nucleotide and amino acid sequences, as presently determined, are reported below for each clone and protein disclosed in the present application. The nucleotide sequence of each clone can readily be determined by sequencing of the deposited clone
15 in accordance with known methods. The predicted amino acid sequence (both full-length and mature forms) can then be determined from such nucleotide sequence. The amino acid sequence of the protein encoded by a particular clone can also be determined by expression of the clone in a suitable host cell, collecting the protein and determining its sequence. For each disclosed protein applicants have identified what they have
20 determined to be the reading frame best identifiable with sequence information available at the time of filing.

As used herein a "secreted" protein is one which, when expressed in a suitable host cell, is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence. "Secreted" proteins include without limitation
25 proteins secreted wholly (e.g., soluble proteins) or partially (e.g., receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins which are transported across the membrane of the endoplasmic reticulum.

Clone "ya15_1"

30 A polynucleotide of the present invention has been identified as clone "ya15_1". ya15_1 was isolated from a human adult testes cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. ya15_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ya15_1 protein").

The nucleotide sequence of ya15_1 as presently determined is reported in SEQ ID NO:1, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the ya15_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:2. Amino acids 8 to 20 of
5 SEQ ID NO:2 are a possible leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 21. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the ya15_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone
10 ya15_1 should be approximately 1100 bp.

The nucleotide sequence disclosed herein for ya15_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ya15_1 demonstrated at least some similarity with sequences identified as Z94056 (Human DNA sequence from PAC 436M11 on chromosome
15 Xp22.11-22.2; contains a serine threonine protein phosphatase gene, ESTs and STSs). Based upon sequence similarity, ya15_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the ya15_1 protein sequence centered around amino acid 40 of SEQ ID NO:2. The nucleotide sequence of ya15_1 indicates that it may contain an
20 Alu repetitive element.

Clone "ya24_1"

A polynucleotide of the present invention has been identified as clone "ya24_1". ya24_1 was isolated from a human adult testes cDNA library and was identified as
25 encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. ya24_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ya24_1 protein").

The nucleotide sequence of ya24_1 as presently determined is reported in SEQ ID NO:3, and includes a poly(A) tail. What applicants presently believe to be the proper
30 reading frame and the predicted amino acid sequence of the ya24_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:4. Amino acids 3 to 15 of SEQ ID NO:4 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 16. Due to the hydrophobic nature of the predicted

leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the ya24_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ya24_1 should be approximately 750 bp.

- 5 The nucleotide sequence disclosed herein for ya24_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ya24_1 demonstrated at least some similarity with sequences identified as AA537299 (vk46d03.r1 Soares mouse mammary gland NbMMG Mus musculus cDNA clone 949637 5'). Based upon sequence similarity, ya24_1 proteins and
10 each similar protein or peptide may share at least some activity.

Clone "yb42_1"

- A polynucleotide of the present invention has been identified as clone "yb42_1". yb42_1 was isolated from a human fetal brain cDNA library and was identified as
15 encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yb42_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yb42_1 protein").

- The nucleotide sequence of yb42_1 as presently determined is reported in SEQ ID NO:5, and includes a poly(A) tail. What applicants presently believe to be the proper
20 reading frame and the predicted amino acid sequence of the yb42_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:6. Amino acids 41 to 53 of SEQ ID NO:6 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 54. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain
25 should the predicted leader/signal sequence not be separated from the remainder of the yb42_1 protein.

- Another potential yb42_1 reading frame and predicted amino acid sequence is encoded by basepairs 1879 to 2220 of SEQ ID NO:5 and is reported in SEQ ID NO:265; amino acids 54 to 66 of SEQ ID NO:265 are a predicted leader/signal sequence, with the
30 predicted mature amino acid sequence beginning at amino acid 67 of SEQ ID NO:265. Due to the hydrophobic nature of this predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO:265.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yb42_1 should be approximately 3900 bp.

The nucleotide sequence disclosed herein for yb42_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yb42_1 demonstrated at least some similarity with sequences identified as AA213992 (zn58d08.s1 Stratagene muscle 937209 Homo sapiens cDNA clone 562383 3'). Based upon sequence similarity, yb42_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of yb42_1 indicates that it may contain at least one MIR repeat sequence.

10

Clone "yc9_1"

A polynucleotide of the present invention has been identified as clone "yc9_1". yc9_1 was isolated from a human fetal kidney (293 cell line) cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yc9_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yc9_1 protein").

The nucleotide sequence of yc9_1 as presently determined is reported in SEQ ID NO:7, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yc9_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:8.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yc9_1 should be approximately 3300 bp.

The nucleotide sequence disclosed herein for yc9_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yc9_1 demonstrated at least some similarity with sequences identified as AA588539 (nm94a07.s1 NCI_CGAP_Co9 Homo sapiens cDNA clone IMAGE:1075860) and N47418 (yy88e12.r1 Homo sapiens cDNA clone 280654 5'). The predicted amino acid sequence disclosed herein for yc9_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted yc9_1 protein demonstrated at least some similarity to sequences identified as X97196 (D. melanogaster X gene). Based upon sequence similarity, yc9_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer

program predicts two potential transmembrane domains within the yc9_1 protein sequence, centered around amino acids 80 and 200 of SEQ ID NO:8, respectively.

Clone "yc19_1"

5 A polynucleotide of the present invention has been identified as clone "yc19_1". yc19_1 was isolated from a human fetal kidney (293 cell line) cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yc19_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as
10 "yc19_1 protein").

The nucleotide sequence of yc19_1 as presently determined is reported in SEQ ID NO:9, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yc19_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:10. Amino acids 106 to
15 118 of SEQ ID NO:10 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 119. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yc19_1 protein.

20 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yc19_1 should be approximately 1400 bp.

The nucleotide sequence disclosed herein for yc19_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yc19_1 demonstrated at least some similarity with sequences
25 identified as AA126002 (zl85a08.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 511382 3') and AA307000 (EST177917 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end). The predicted amino acid sequence disclosed herein for yc19_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted yc19_1 protein demonstrated at least some
30 similarity to sequences identified as X83742 (MAP kinase phosphatase [Xenopus laevis]), and to several tyrosine phosphatases from other species. Based upon sequence similarity, yc19_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional potential transmembrane domain within the yc19_1 protein sequence centered around amino acid 43 of SEQ ID NO:10; this

region (amino acids 30 to 42 of SEQ ID NO:10) may also be a leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 43.

yc19_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 23 kDa was detected in conditioned medium and
5 membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "yc20_1"

A polynucleotide of the present invention has been identified as clone "yc20_1". yc20_1 was isolated from a human fetal kidney (293 cell line) cDNA library and was
10 identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yc20_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yc20_1 protein").

The nucleotide sequence of yc20_1 as presently determined is reported in SEQ ID
15 NO:11, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yc20_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:12.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yc20_1 should be approximately 1450 bp.

20 The nucleotide sequence disclosed herein for yc20_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yc20_1 demonstrated at least some similarity with sequences identified as AA447839 (aa18c12.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 813622 5'), N33405 (yy41e10.s1 Homo sapiens cDNA clone 273834 3'), and T19519 (Human
25 gene signature HUMGS00580). Based upon sequence similarity, yc20_1 proteins and each similar protein or peptide may share at least some activity.

Clone "ya9_1"

A polynucleotide of the present invention has been identified as clone "ya9_1".
30 ya9_1 was isolated from a human adult testes cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. ya9_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ya9_1 protein").

The nucleotide sequence of ya9_1 as presently determined is reported in SEQ ID NO:13, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the ya9_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:14. Amino acids 15 to 27 of SEQ ID NO:14 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 28. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the ya9_1 protein.

10 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ya9_1 should be approximately 950 bp.

The nucleotide sequence disclosed herein for ya9_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ya9_1 demonstrated at least some similarity with sequences identified as AA442366 (zv62c04.r1 Soares testis NHT Homo sapiens cDNA clone 758214 5') and AA609166 (af12a08.s1 Soares testis NHT Homo sapiens cDNA clone 1031414 3'). Based upon sequence similarity, ya9_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional potential transmembrane domain within the ya9_1 protein sequence, centered around amino acid 62 of SEQ ID NO:14.

Clone "ya11_1"

A polynucleotide of the present invention has been identified as clone "ya11_1". ya11_1 was isolated from a human adult testes cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. ya11_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ya11_1 protein").

The nucleotide sequence of ya11_1 as presently determined is reported in SEQ ID NO:15, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the ya11_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:16. Amino acids 36 to 48 of SEQ ID NO:16 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 49. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should

the predicted leader/signal sequence not be separated from the remainder of the ya11_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ya11_1 should be approximately 500 bp.

- 5 The nucleotide sequence disclosed herein for ya11_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ya11_1 demonstrated at least some similarity with sequences identified as Z68274 (Human DNA sequence from cosmid L129H7, Huntington's Disease Region, chromosome 4p16.3 contains Pseudogene and CpG island). Based upon sequence
10 similarity, ya11_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional potential transmembrane domain within the ya11_1 protein sequence, centered around amino acid 81 of SEQ ID NO:16.

15 Clone "ya28_1"

- A polynucleotide of the present invention has been identified as clone "ya28_1". ya28_1 was isolated from a human adult testes cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. ya28_1 is a full-length clone, including the
20 entire coding sequence of a secreted protein (also referred to herein as "ya28_1 protein").

- The nucleotide sequence of ya28_1 as presently determined is reported in SEQ ID NO:17, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the ya28_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:18. Amino acids 41 to 53
25 of SEQ ID NO:18 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 54. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the ya28_1 protein.

- 30 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ya28_1 should be approximately 300 bp.

The nucleotide sequence disclosed herein for ya28_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ya28_1 demonstrated at least some similarity with sequences

identified as AA576255 (nm62b09.s1 NCI_CGAP_Br3 Homo sapiens cDNA clone IMAGE:1072793). Based upon sequence similarity, ya28_1 proteins and each similar protein or peptide may share at least some activity.

- 5 ya28_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 23 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "yb81_1"

- A polynucleotide of the present invention has been identified as clone "yb81_1".
- 10 yb81_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yb81_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yb81_1 protein").

- The nucleotide sequence of yb81_1 as presently determined is reported in SEQ ID NO:19, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yb81_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:20.
- 15

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yb81_1 should be approximately 1200 bp.

- 20 The nucleotide sequence disclosed herein for yb81_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yb81_1 demonstrated at least some similarity with sequences identified as T67164 (Human alpha-N-acetylglucosaminidase gene). Based upon sequence similarity, yb81_1 proteins and each similar protein or peptide may share at least some
- 25 activity. The TopPredII computer program predicts a potential transmembrane domain within the yb81_1 protein sequence centered around amino acid 73 of SEQ ID NO:20.

Clone "yc14_1"

- A polynucleotide of the present invention has been identified as clone "yc14_1".
- 30 yc14_1 was isolated from a human fetal kidney (293 cell line) cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yc14_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yc14_1 protein").

The nucleotide sequence of yc14_1 as presently determined is reported in SEQ ID NO:21, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yc14_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:22. Amino acids 388 to 400 of SEQ ID NO:22 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 401. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yc14_1 protein.

10 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yc14_1 should be approximately 3000 bp.

The nucleotide sequence disclosed herein for yc14_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yc14_1 demonstrated at least some similarity with sequences identified as AA007392 (zh99a08.r1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 429398 5'), AA573120 (nj41e10.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE 995082 similar to TR G285999 G285999 ORF, COMPLETE CDS), and D13642 (Human mRNA for KIAA0017 gene, complete cds). The predicted amino acid sequence disclosed herein for yc14_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted yc14_1 protein demonstrated at least some similarity to sequences identified as D13642 (KIAA0017 [Homo sapiens]) and Z47816 (unknown [Saccharomyces cerevisiae] (S. cerevisiae chromosome XIII cosmid 9827, and translated products)). The yc14_1 protein contains the immunoglobulin and major histocompatibility complex protein signature at its extreme N-terminus (starting at amino acid 3 of SEQ ID NO:22). Based upon sequence similarity, yc14_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts four additional potential transmembrane domains within the yc14_1 protein sequence, centered around amino acids 50, 200, 210, and 830 of SEQ ID NO:22, respectively.

30 yc14_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 92 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "yc24_1"

A polynucleotide of the present invention has been identified as clone "yc24_1". yc24_1 was isolated from a human fetal kidney (293 cell line) cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer
5 analysis of the amino acid sequence of the encoded protein. yc24_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yc24_1 protein").

The nucleotide sequence of yc24_1 as presently determined is reported in SEQ ID NO:23, and includes a poly(A) tail. What applicants presently believe to be the proper
10 reading frame and the predicted amino acid sequence of the yc24_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:24. Amino acids 50 to 62 of SEQ ID NO:24 are a possible leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 63. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted
15 leader/signal sequence not be separated from the remainder of the yc24_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yc24_1 should be approximately 1650 bp.

The nucleotide sequence disclosed herein for yc24_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and
20 FASTA search protocols. yc24_1 demonstrated at least some similarity with sequences identified as AA172170 (zp29b07.s1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone 610837 3' similar to gb L10240 BASIGIN PRECURSOR (HUMAN), AA756004 (vv37a04.r1 Stratagene mouse heart (#937316) Mus musculus cDNA clone 1224558 5' similar to TR:Q14134 Q14134 ATAXIA-TELANGIECTASIA GROUP D-ASSOCIATED
25 PROTEIN, mRNA sequence), D48379 (Rice cDNA, partial sequence (S14546_1A), mRNA sequence), E07941 (cDNA encoding human basigin1), L20471 (Human extracellular matrix metalloproteinase inducer gene, complete cds), Q71341 (Human basigin I immunoglobulin gene), and X64364 (H.sapiens mRNA for M6 antigen). The M6 antigen has been localized in all leucocyte lines examined (including lymphocytes, monocytes, and granulocytes) and
30 is implicated in interacting with cytokine factors like GM-CSF and interferon gamma. A protein that is at least very similar to M6 antigen, extracellular matrix metalloproteinase inducer (EMMPRIN), has been localized to the surface of tumor cells and is implicated in stimulating several matrix metalloproteinases in the fibroblasts. Based upon sequence similarity, yc24_1 proteins and each similar protein or peptide may share at least some

activity. The TopPredII computer program predicts a potential transmembrane domain within the yc24_1 protein sequence near the N-terminus of SEQ ID NO:24.

Clone "yc25_1"

5 A polynucleotide of the present invention has been identified as clone "yc25_1". yc25_1 was isolated from a human fetal kidney (293 cell line) cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yc25_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as
10 "yc25_1 protein").

The nucleotide sequence of yc25_1 as presently determined is reported in SEQ ID NO:25, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yc25_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:26. Amino acids 6 to 18
15 of SEQ ID NO:26 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 19. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yc25_1 protein.

20 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yc25_1 should be approximately 1800 bp.

The nucleotide sequence disclosed herein for yc25_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yc25_1 demonstrated at least some similarity with sequences
25 identified as AA332406 (EST36341 Embryo, 8 week I Homo sapiens cDNA 5' end), T20094 (Human gene signature HUMGS01237), and W73912 (zd71a11.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 346076 3'). Based upon sequence similarity, yc25_1 proteins and each similar protein or peptide may share at least some activity.

30 Clone "ye2_1"

A polynucleotide of the present invention has been identified as clone "ye2_1". ye2_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid

sequence of the encoded protein. ye2_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ye2_1 protein").

The nucleotide sequence of ye2_1 as presently determined is reported in SEQ ID NO:27, and includes a poly(A) tail. What applicants presently believe to be the proper
5 reading frame and the predicted amino acid sequence of the ye2_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:28. Amino acids 30 to 42 of SEQ ID NO:28 are a possible leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 43. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted
10 leader/signal sequence not be separated from the remainder of the ye2_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ye2_1 should be approximately 1500 bp.

The nucleotide sequence disclosed herein for ye2_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and
15 FASTA search protocols. ye2_1 demonstrated at least some similarity with sequences identified as AA354797 (EST63132 Jurkat T-cells V Homo sapiens cDNA 5' end) and Z43858 (H. sapiens partial cDNA sequence; clone c-1md12). Based upon sequence similarity, ye2_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional potential trans-
20 membrane domain within the ye2_1 protein sequence centered around amino acid 70 of SEQ ID NO:28.

Clone "ya65_1"

A polynucleotide of the present invention has been identified as clone "ya65_1".
25 ya65_1 was isolated from a human adult testes cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. ya65_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ya65_1 protein").

The nucleotide sequence of ya65_1 as presently determined is reported in SEQ ID
30 NO:29, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the ya65_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:30.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ya65_1 should be approximately 550 bp.

The nucleotide sequence disclosed herein for ya65_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ya65_1 demonstrated at least some similarity with sequences identified as AI005084 (ou08g10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
5 IMAGE:1625730 3', mRNA sequence). Based upon sequence similarity, ya65_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the ya65_1 protein sequence centered around amino acid 87 of SEQ ID NO:30.

10 Clone "yb60_1"

A polynucleotide of the present invention has been identified as clone "yb60_1". yb60_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yb60_1 is a full-length clone, including the
15 entire coding sequence of a secreted protein (also referred to herein as "yb60_1 protein").

The nucleotide sequence of yb60_1 as presently determined is reported in SEQ ID NO:31, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yb60_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:32. Amino
20 acids 46 to 58 of SEQ ID NO:32 are a possible leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 59. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yb60_1 protein.

25 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yb60_1 should be approximately 2500 bp.

The nucleotide sequence disclosed herein for yb60_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yb60_1 demonstrated at least some similarity with sequences
30 identified as AA505869 (nh99f02.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:966651), H29487 (ym60a10.r1 Homo sapiens cDNA clone 52621 5'), and T24510 (Human gene signature HUMGS06552; standard; cDNA to mRNA). Based upon sequence similarity, yb60_1 proteins and each similar protein or peptide may share at least some activity.

Clone "yb139_1"

A polynucleotide of the present invention has been identified as clone "yb139_1". yb139_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yb139_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yb139_1 protein").

The nucleotide sequence of yb139_1 as presently determined is reported in SEQ ID NO:33, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yb139_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:34. Amino acids 101 to 113 of SEQ ID NO:34 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 114. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yb139_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yb139_1 should be approximately 1000 bp.

The nucleotide sequence disclosed herein for yb139_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yb139_1 demonstrated at least some similarity with sequences identified as AA332206 (EST36115 Embryo, 8 week I Homo sapiens cDNA 5' end, mRNA sequence). Based upon sequence similarity, yb139_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional potential transmembrane domain within the yb139_1 protein sequence centered around amino acid 42 of SEQ ID NO:34. The nucleotide acid sequence of yb139_1 indicates that it may contain sequences similar to a primate simple repeat and to the *M. serrator* retropseudogene-like repetitive element I.

Clone "yc29_1"

A polynucleotide of the present invention has been identified as clone "yc29_1". yc29_1 was isolated from a human fetal kidney (293 cell line) cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yc29_1 is a full-length clone,

including the entire coding sequence of a secreted protein (also referred to herein as "yc29_1 protein").

The nucleotide sequence of yc29_1 as presently determined is reported in SEQ ID NO:35, and includes a poly(A) tail. What applicants presently believe to be the proper
5 reading frame and the predicted amino acid sequence of the yc29_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:36.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yc29_1 should be approximately 2100 bp.

The nucleotide sequence disclosed herein for yc29_1 was searched against the
10 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yc29_1 demonstrated at least some similarity with sequences identified as AA195033 (zr35a12.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 665374 3', mRNA sequence), AF046001 (Homo sapiens zinc finger transcription factor (ZNF207) mRNA, complete cds), and T23300 (Human gene signature HUMGS05114; standard;
15 cDNA to mRNA). The predicted amino acid sequence disclosed herein for yc29_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted yc29_1 protein demonstrated at least some similarity to the sequence identified as AF046001 (zinc finger transcription factor [Homo sapiens]). The presence of zinc fingers in a protein may indicate that the protein has a
20 DNA-binding function, but zinc fingers may also be protein-protein interaction domains. Based upon sequence similarity, yc29_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two potential transmembrane domains within the yc29_1 protein sequence, one centered around amino acid 175 and another around amino acid 210 of SEQ ID NO:36.

25 yc29_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 56 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "yc40_1"

30 A polynucleotide of the present invention has been identified as clone "yc40_1". yc40_1 was isolated from a human fetal kidney (293 cell line) cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yc40_1 is a full-length clone,

including the entire coding sequence of a secreted protein (also referred to herein as "yc40_1 protein").

The nucleotide sequence of yc40_1 as presently determined is reported in SEQ ID NO:37, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yc40_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:38. Amino acids 31 to 43 of SEQ ID NO:38 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 44. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yc40_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yc40_1 should be approximately 1400 bp.

The nucleotide sequence disclosed herein for yc40_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yc40_1 demonstrated at least some similarity with sequences identified as D62445 (Human aorta cDNA 5'-end GEN-286A10, mRNA sequence) and T25162 (Human gene signature HUMGS07322; standard; DNA). Based upon sequence similarity, yc40_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the yc40_1 protein sequence centered around amino acid 50 of SEQ ID NO:38.

Clone "yd10_1"

A polynucleotide of the present invention has been identified as clone "yd10_1". yd10_1 was isolated from a human adult brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yd10_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yd10_1 protein").

The nucleotide sequence of yd10_1 as presently determined is reported in SEQ ID NO:39, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yd10_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:40. Amino acids 47 to 59 of SEQ ID NO:40 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 60. Due to the hydrophobic nature

of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yd10_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone
5 yd10_1 should be approximately 825 bp.

The nucleotide sequence disclosed herein for yd10_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yd10_1 demonstrated at least some similarity with sequences identified as AA587270 (nn70g03.s1 NCI_CGAP_Lar1 Homo sapiens cDNA clone
10 IMAGE:1089268 similar to contains Alu repetitive element; contains element PTR5 repetitive element; mRNA sequence). Based upon sequence similarity, yd10_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of yd10_1 indicates that it may contain an Alu repetitive element.

15 Clone "yf5_1"

A polynucleotide of the present invention has been identified as clone "yf5_1". yf5_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yf5_1 is a full-length clone, including the entire coding
20 sequence of a secreted protein (also referred to herein as "yf5_1 protein").

The nucleotide sequence of yf5_1 as presently determined is reported in SEQ ID NO:41, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yf5_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:42. Amino acids 9 to 21
25 of SEQ ID NO:42 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 22. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yf5_1 protein.

30 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yf5_1 should be approximately 1800 bp.

The nucleotide sequence disclosed herein for yf5_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yf5_1 demonstrated at least some similarity with sequences

identified as AA181631 (zp52a03.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone 613036 3', mRNA sequence) and U49082 (Human transporter protein (g17) mRNA, complete cds). The predicted amino acid sequence disclosed herein for yf5_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted yf5_1 protein demonstrated at least some similarity to the sequence identified as U49082 (transporter protein [Homo sapiens]). Based upon sequence similarity, yf5_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts ten additional potential transmembrane domains within the yf5_1 protein sequence, centered around amino acids 36, 84, 130, 154, 213, 249, 292, 330, 353, and 389 of SEQ ID NO:42, respectively. The nucleotide sequence of yf5_1 indicates that it may contain a MIR repeat region.

Clone "ya67_1"

A polynucleotide of the present invention has been identified as clone "ya67_1". ya67_1 was isolated from a human adult testes cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. ya67_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ya67_1 protein").

The nucleotide sequence of ya67_1 as presently determined is reported in SEQ ID NO:43, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the ya67_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:44. Amino acids 14 to 26 of SEQ ID NO:44 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 27. Amino acids 16 to 28 are also a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 29. Due to the hydrophobic nature of the predicted leader/signal sequences, each is likely to act as a transmembrane domain should it not be separated from the remainder of the ya67_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ya67_1 should be approximately 800 bp.

The nucleotide sequence disclosed herein for ya67_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ya67_1 demonstrated at least some similarity with sequences identified as AC002042 (**SEQUENCING IN PROGRESS**) Homo sapiens chromosome

16p11.2 BAC clone CIT987SK-A-180G2; HTGS phase 1, 5 unordered pieces). Based upon sequence similarity, ya67_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of ya67_1 indicates that it may contain an MIR repeat sequence.

- 5 ya67_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 21 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "ya70_1"

- 10 A polynucleotide of the present invention has been identified as clone "ya70_1". ya70_1 was isolated from a human adult testes cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. ya70_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ya70_1 protein").

- 15 The nucleotide sequence of ya70_1 as presently determined is reported in SEQ ID NO:45, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the ya70_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:46.

- The EcoRI/NotI restriction fragment obtainable from the deposit containing clone
20 ya70_1 should be approximately 1500 bp.

- The nucleotide sequence disclosed herein for ya70_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ya70_1 demonstrated at least some similarity with sequences identified as AA813657 (ai69c03.s1 Soares testis NHT Homo sapiens cDNA clone 1376068
25 3', mRNA sequence) and U84408 (Human IL-1 receptor related protein MyD88 mRNA, complete cds). The predicted amino acid sequence disclosed herein for ya70_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted ya70_1 protein demonstrated at least some similarity to the sequences identified as U84408 (MyD88 [Homo sapiens]). Human
30 MyD88, an IL-6 primary response gene, encodes a protein containing an N-terminal death domain and a C-terminal region that exhibits homology to human IL-1Rp80 and drosophila Toll (IL-1Rp80 and Toll are homologs). Based upon sequence similarity, ya70_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two potential transmembrane domains within the

ya70_1 protein sequence, one centered around amino acid 90 and another around amino acid 175 of SEQ ID NO:46.

Clone "yb51_1"

5 A polynucleotide of the present invention has been identified as clone "yb51_1". yb51_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yb51_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yb51_1 protein").

10 The nucleotide sequence of yb51_1 as presently determined is reported in SEQ ID NO:47, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yb51_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:48. Amino acids 5 to 17 of SEQ ID NO:48 are a predicted leader/signal sequence, with the predicted
15 mature amino acid sequence beginning at amino acid 18. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yb51_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone
20 yb51_1 should be approximately 1400 bp.

The nucleotide sequence disclosed herein for yb51_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yb51_1 demonstrated at least some similarity with sequences identified as AA058715 (zk70c03.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA
25 clone 488164 3' similar to contains Alu repetitive element; contains element MER1 repetitive element) and Z44795 (H. sapiens partial cDNA sequence; clone c-29d08). Based upon sequence similarity, yb51_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional potential transmembrane domain within the yb51_1 protein sequence centered around amino acid
30 59 of SEQ ID NO:48. The nucleotide sequence of yb51_1 indicates that it may contain at least one repetitive element.

Clone "yb101_1"

A polynucleotide of the present invention has been identified as clone "yb101_1". yb101_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yb101_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yb101_1 protein").

The nucleotide sequence of yb101_1 as presently determined is reported in SEQ ID NO:49, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yb101_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:50.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yb101_1 should be approximately 1050 bp.

The nucleotide sequence disclosed herein for yb101_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yb101_1 demonstrated at least some similarity with sequences identified as AC005060 (Homo sapiens clone RG086D03; HTGS phase 1, 3 unordered pieces) and D60925 (Human fetal brain cDNA 5'-end GEN-139D01, mRNA sequence). Based upon sequence similarity, yb101_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the yb101_1 protein sequence centered around amino acid 11 of SEQ ID NO:50.

yb101_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 8 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "yb124_1"

A polynucleotide of the present invention has been identified as clone "yb124_1". yb124_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yb124_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yb124_1 protein").

The nucleotide sequence of yb124_1 as presently determined is reported in SEQ ID NO:51, and includes a poly(A) tail. What applicants presently believe to be the proper

reading frame and the predicted amino acid sequence of the yb124_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:52.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yb124_1 should be approximately 1700 bp.

5 The nucleotide sequence disclosed herein for yb124_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yb124_1 demonstrated at least some similarity with sequences identified as AA430306 (zw68g03.r1 Soares testis NHT Homo sapiens cDNA clone 781396 5', mRNA sequence). Based upon sequence similarity, yb124_1 proteins and each similar
10 protein or peptide may share at least some activity. The TopPredII computer program predicts three potential transmembrane domains within the yb124_1 protein sequence, centered around amino acids 30, 84, and 134 of SEQ ID NO:52, respectively. Amino acids 128 to 140 of SEQ ID NO:52 also have characteristics indicative of a leader/signal sequence.

15

Clone "yb125_1"

A polynucleotide of the present invention has been identified as clone "yb125_1". yb125_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the
20 amino acid sequence of the encoded protein. yb125_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yb125_1 protein").

The nucleotide sequence of yb125_1 as presently determined is reported in SEQ ID NO:53, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yb125_1 protein
25 corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:54. Amino acids 15 to 27 of SEQ ID NO:54 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 28. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the
30 yb125_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yb125_1 should be approximately 2000 bp.

The nucleotide sequence disclosed herein for yb125_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and

FASTA search protocols. yb125_1 demonstrated at least some similarity with sequences identified as AA340207 (EST45465 Fetal brain III Homo sapiens cDNA 5' end, mRNA sequence) and Q92781 (Human thymopoietin gene fragment; standard; DNA). Based upon sequence similarity, yb125_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of yb125_1 indicates that it may contain an Alu repetitive element.

Clone "yb179_1"

A polynucleotide of the present invention has been identified as clone "yb179_1". yb179_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yb179_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yb179_1 protein").

The nucleotide sequence of yb179_1 as presently determined is reported in SEQ ID NO:55, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yb179_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:56.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yb179_1 should be approximately 1500 bp.

The nucleotide sequence disclosed herein for yb179_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yb179_1 demonstrated at least some similarity with sequences identified as AA398428 (zt62a11.s1 Soares testis NHT Homo sapiens cDNA clone 726908 3', mRNA sequence). Based upon sequence similarity, yb179_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the yb179_1 protein sequence centered around amino acid 100 of SEQ ID NO:56. Amino acids 97 to 109 of SEQ ID NO:56 are also a possible leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 110.

Clone "yc48_1"

A polynucleotide of the present invention has been identified as clone "yc48_1". yc48_1 was isolated from a human fetal kidney (293 cell line) cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer

analysis of the amino acid sequence of the encoded protein. yc48_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yc48_1 protein").

The nucleotide sequence of yc48_1 as presently determined is reported in SEQ ID NO:57, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yc48_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:58. Amino acids 5 to 17 of SEQ ID NO:58 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 18. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yc48_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yc48_1 should be approximately 1400 bp.

The nucleotide sequence disclosed herein for yc48_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yc48_1 demonstrated at least some similarity with sequences identified as AI009170 (EST203621 Normalized rat embryo, Bento Soares Rattus sp. cDNA clone REMBJ87 3' end, mRNA sequence). Based upon sequence similarity, yc48_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two additional potential transmembrane domains within the yc48_1 protein sequence, one centered around amino acid 110 and another around amino acid 180 of SEQ ID NO:58.

Clone "ye21_1"

A polynucleotide of the present invention has been identified as clone "ye21_1". ye21_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. ye21_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ye21_1 protein").

The nucleotide sequence of ye21_1 as presently determined is reported in SEQ ID NO:59, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the ye21_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:60. Amino acids 9 to 21

of SEQ ID NO:60 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 22. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the ye21_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ye21_1 should be approximately 1550 bp.

The nucleotide sequence disclosed herein for ye21_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No significant hits were found in the databases. The TopPredII computer program predicts a potential transmembrane domain within the ye21_1 protein sequence centered around amino acid 66 of SEQ ID NO:60. The nucleotide sequence of ye21_1 indicates that it may contain an Alu repetitive element.

Clone "ye22_1"

A polynucleotide of the present invention has been identified as clone "ye22_1". ye22_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. ye22_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ye22_1 protein").

The nucleotide sequence of ye22_1 as presently determined is reported in SEQ ID NO:61, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the ye22_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:62.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ye22_1 should be approximately 1600 bp.

The nucleotide sequence disclosed herein for ye22_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ye22_1 demonstrated at least some similarity with sequences identified as AJ002553 (** SEQUENCING IN PROGRESS ** Homo sapiens genomic DNA (PAC 1118i22) from chromosome 11; HTGS phase 1) and T19813 (Human gene signature HUMGS00891; standard; cDNA to mRNA). The predicted amino acid sequence disclosed herein for ye22_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted ye22_1 protein

demonstrated at least some similarity to the sequence identified as AF003145 (No definition line found [Caenorhabditis elegans]). Based upon sequence similarity, ye22_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the
5 ye22_1 protein sequence centered around amino acid 77 of SEQ ID NO:62. The nucleotide sequence of ye22_1 indicates that it may contain repetitive elements.

Clone "ye39_1"

A polynucleotide of the present invention has been identified as clone "ye39_1".
10 ye39_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. ye39_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ye39_1 protein").

The nucleotide sequence of ye39_1 as presently determined is reported in SEQ ID
15 NO:63, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the ye39_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:64.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ye39_1 should be approximately 1700 bp.

20 The nucleotide sequence disclosed herein for ye39_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ye39_1 demonstrated at least some similarity with sequences identified as AA360300 (EST69467 Liver II Homo sapiens cDNA 5' end, mRNA sequence). Based upon sequence similarity, ye39_1 proteins and each similar protein or peptide may
25 share at least some activity. The TopPredII computer program predicts two potential transmembrane domains within the ye39_1 protein sequence, one centered around amino acid 20 and another around amino acid 45 of SEQ ID NO:64.

Clone "yf9_1"

30 A polynucleotide of the present invention has been identified as clone "yf9_1". yf9_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yf9_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yf9_1 protein").

The nucleotide sequence of yf9_1 as presently determined is reported in SEQ ID NO:65. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yf9_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:66.

- 5 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yf9_1 should be approximately 950 bp.

The nucleotide sequence disclosed herein for yf9_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yf9_1 demonstrated at least some similarity with sequences
10 identified as AA747796 (nx86a03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE 1269100, mRNA sequence) and AF009426 (Homo sapiens clone 22 mRNA, alternative splice variant beta-1, complete cds). The predicted amino acid sequence disclosed herein for yf9_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted yf9_1 protein
15 demonstrated at least some similarity to the sequence identified as AF009426 (clone 22 [Homo sapiens]). Based upon sequence similarity, yf9_1 proteins and each similar protein or peptide may share at least some activity. Clone 22 mRNA was identified from brain transcripts and the corresponding gene has been localized to chromosome 18; the chromosome regions 18p and 18q where the transcripts cluster are candidate regions for
20 bipolar disorder. The protein products of the clone 22 mRNA variants are predicted to be membrane spanning. (Yoshikawa *et al.*, 1997, *Am. J. Med. Genet.* 74(2): 140-149, which is incorporated by reference herein). The predicted yf9_1 protein appears to be a novel splice variant expressed from the clone 22 gene. The TopPredII computer program predicts a potential transmembrane domain within the yf9_1 protein sequence centered
25 around amino acid 39 of SEQ ID NO:66.

yf9_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 24 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

30 Clone "yh4_1"

A polynucleotide of the present invention has been identified as clone "yh4_1". yh4_1 was isolated from a human brain (fetal and adult) cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the

amino acid sequence of the encoded protein. yh4_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yh4_1 protein").

The nucleotide sequence of yh4_1 as presently determined is reported in SEQ ID NO:67, and includes a poly(A) tail. What applicants presently believe to be the proper
5 reading frame and the predicted amino acid sequence of the yh4_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:68.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yh4_1 should be approximately 1500 bp.

The nucleotide sequence disclosed herein for yh4_1 was searched against the
10 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No significant hits were found in the databases. The TopPredII computer program predicts a potential transmembrane domain within the yh4_1 protein sequence centered around amino acid 80 of SEQ ID NO:68. The nucleotide sequence of yh4_1 indicates that it may contain an Alu repetitive element.

15

Clone "yi4_1"

A polynucleotide of the present invention has been identified as clone "yi4_1". yi4_1 was isolated from a human brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid
20 sequence of the encoded protein. yi4_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yi4_1 protein").

The nucleotide sequence of yi4_1 as presently determined is reported in SEQ ID NO:69, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yi4_1 protein corresponding
25 to the foregoing nucleotide sequence is reported in SEQ ID NO:70. Amino acids 18 to 30 of SEQ ID NO:70 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 31. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yi4_1
30 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yi4_1 should be approximately 1400 bp.

The nucleotide sequence disclosed herein for yi4_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and

FASTA search protocols. yi4_1 demonstrated at least some similarity with sequences identified as AA553835 (nk94f03.s1 NCI_CGAP_Co11 Homo sapiens cDNA clone IMAGE:1028477, mRNA sequence) and T22931 (Human gene signature HUMGS04656; standard; cDNA to mRNA). Based upon sequence similarity, yi4_1 proteins and each
5 similar protein or peptide may share at least some activity. The nucleotide sequence of yi4_1 indicates that it may contain simple nucleotide repeat sequences.

Clone "yj3_1"

A polynucleotide of the present invention has been identified as clone "yj3_1".
10 yj3_1 was isolated from a human fetal kidney (293 cell line) cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yj3_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yj3_1 protein").

15 The nucleotide sequence of yj3_1 as presently determined is reported in SEQ ID NO:71, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yj3_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:72. Amino acids 8 to 20 of SEQ ID NO:72 are a predicted leader/signal sequence, with the predicted mature
20 amino acid sequence beginning at amino acid 21. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yj3_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone
25 yj3_1 should be approximately 900 bp.

The nucleotide sequence disclosed herein for yj3_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yj3_1 demonstrated at least some similarity with sequences identified as AC004955 (Homo sapiens clone DJ1087M19; HTGS phase 1, 7 unordered
30 pieces) and W37665 (zc12f05.r1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 322113 5', mRNA sequence). Based upon sequence similarity, yj3_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts four additional potential transmembrane domains within the yj3_1

protein sequence, centered around amino acids 17, 45, 87, and 110 of SEQ ID NO:72, respectively.

Clone "yj7_1"

5 A polynucleotide of the present invention has been identified as clone "yj7_1". yj7_1 was isolated from a human fetal kidney (293 cell line) cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yj7_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yj7_1
10 protein").

The nucleotide sequence of yj7_1 as presently determined is reported in SEQ ID NO:73, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yj7_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:74. Amino acids 21 to 33
15 of SEQ ID NO:74 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 34. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yj7_1 protein.

20 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yj7_1 should be approximately 1159 bp.

The nucleotide sequence disclosed herein for yj7_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yj7_1 demonstrated at least some similarity with sequences
25 identified as AA827998 (of10c11.s1 NCI_CGAP_Co12 Homo sapiens cDNA clone IMAGE:1420724 3', mRNA sequence), C80074 (Mus musculus 3.5-dpc blastocyst cDNA 3'-end sequence, mRNA sequence), and T25792 (Human gene signature HUMGS08020; standard; cDNA to mRNA). The predicted amino acid sequence disclosed herein for yj7_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the
30 BLASTX search protocol. The predicted yj7_1 protein demonstrated at least some similarity to sequences identified as R61477 (Clavulanic acid dehydrogenase sequence), U43283 (similar to the insect-type alcohol dehydrogenase/ribitol dehydrogenase family [Caenorhabditis elegans]), and Z99116 (similar to ketoacyl reductase[Bacillus subtilus]). Based upon sequence similarity, yj7_1 proteins and each similar protein or peptide may

share at least some activity. Motifs search revealed the short-chain alcohol dehydrogenase family signature. These dehydrogenases and reductases are cytoplasmic, however, the amino acid similarity alignment is more consistent with domain/motif sharing. Also, the predicted yj7_1 protein demonstrates similarity to proteins that are only "similar to" these dehydrogenase and reductase enzymes; the predicted yj7_1 protein exhibits less amino-acid similarity to the enzymes themselves. Therefore, the predicted yj7_1 protein might be a novel, secreted form of alcohol dehydrogenase.

yj7_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 32 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "yj10_1"

A polynucleotide of the present invention has been identified as clone "yj10_1". yj10_1 was isolated from a human fetal kidney (293 cell line) cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yj10_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yj10_1 protein").

The nucleotide sequence of yj10_1 as presently determined is reported in SEQ ID NO:75, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yj10_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:76.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yj10_1 should be approximately 1600 bp.

The nucleotide sequence disclosed herein for yj10_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yj10_1 demonstrated at least some similarity with sequences identified as AF072860 (Homo sapiens protein activator of the interferon-induced protein kinase (PACT) mRNA, complete cds), AI056368 (oy48c07.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE 1669068 3' similar to TR Q91836 Q91836 RNA BINDING PROTEIN; mRNA sequence) and T24520 (Human gene signature HUMGS06564; standard; cDNA to mRNA). The predicted amino acid sequence disclosed herein for yj10_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted yj10_1 protein demonstrated at least

some similarity to the sequence identified as AF072860 (protein activator of the interferon-induced protein kinase [Homo sapiens]). Based upon sequence similarity, yj10_1 proteins and each similar protein or peptide may share at least some activity.

5 Clone "yj28_1"

A polynucleotide of the present invention has been identified as clone "yj28_1". yj28_1 was isolated from a human fetal kidney (293 cell line) cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yj28_1 is a full-length clone,
10 including the entire coding sequence of a secreted protein (also referred to herein as "yj28_1 protein").

The nucleotide sequence of yj28_1 as presently determined is reported in SEQ ID NO:77, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yj28_1 protein corresponding
15 to the foregoing nucleotide sequence is reported in SEQ ID NO:78. Amino acids 160 to 172 of SEQ ID NO:78 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 173. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yj28_1
20 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yj28_1 should be approximately 1250 bp.

The nucleotide sequence disclosed herein for yj28_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and
25 FASTA search protocols. yj28_1 demonstrated at least some similarity with sequences identified as AA402090 (zu53f03.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 741725 5', mRNA sequence) and AJ009691 (Podocoryne carnea mRNA for SMC2orf protein, partial). The predicted amino acid sequence disclosed herein for yj28_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the
30 BLASTX search protocol. The predicted yj28_1 protein demonstrated at least some similarity to the sequence identified as AJ009691 (SMC2orf [Podocoryne carnea]). Based upon sequence similarity, yj28_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional potential

transmembrane domain within the yj28_1 protein sequence centered around amino acid 348 of SEQ ID NO:78.

Clone "yj29_1"

5 A polynucleotide of the present invention has been identified as clone "yj29_1". yj29_1 was isolated from a human fetal kidney (293 cell line) cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yj29_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as
10 "yj29_1 protein").

The nucleotide sequence of yj29_1 as presently determined is reported in SEQ ID NO:79, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yj29_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:80. Amino acids 310 to
15 322 of SEQ ID NO:80 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 323. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yj29_1 protein.

20 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yj29_1 should be approximately 1600 bp.

The nucleotide sequence disclosed herein for yj29_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yj29_1 demonstrated at least some similarity with sequences
25 identified as AA156900 (zl20c06.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 502474 5' similar to WP:T06D8.8 CE02329; mRNA sequence), AF015416 (Homo sapiens chromosome 11 from 11p15.5 region, complete sequence), and T23342 Human gene signature HUMGS05162; standard; cDNA to mRNA). The predicted amino acid sequence disclosed herein for yj29_1 was searched against the GenPept and GeneSeq
30 amino acid sequence databases using the BLASTX search protocol. The predicted yj29_1 protein demonstrated at least some similarity to the sequence identified as Z49130 (T06D8.8 [Caenorhabditis elegans]). Based upon sequence similarity, yj29_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer

program predicts an additional potential transmembrane domain within the yj29_1 protein sequence centered around amino acid 207 of SEQ ID NO:80.

Clone "yj32_1"

5 A polynucleotide of the present invention has been identified as clone "yj32_1". yj32_1 was isolated from a human fetal kidney (293 cell line) cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yj32_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as
10 "yj32_1 protein").

The nucleotide sequence of yj32_1 as presently determined is reported in SEQ ID NO:81, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yj32_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:82. Amino acids 64 to 76
15 of SEQ ID NO:82 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 77. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yj32_1 protein.

20 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yj32_1 should be approximately 1450 bp.

The nucleotide sequence disclosed herein for yj32_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No significant hits were found in the databases. The TopPredII
25 computer program predicts an additional potential transmembrane domain within the yj32_1 protein sequence, near the N-terminus of SEQ ID NO:82. The nucleotide sequence of yj32_1 indicates that it may contain an Alu repetitive element.

yj32_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 10 kDa was detected in conditioned medium using SDS
30 polyacrylamide gel electrophoresis.

Clone "yb186_1"

A polynucleotide of the present invention has been identified as clone "yb186_1". yb186_1 was isolated from a human fetal brain cDNA library and was identified as

encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yb186_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yb186_1 protein").

The nucleotide sequence of yb186_1 as presently determined is reported in SEQ ID NO:83, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yb186_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:84. Amino acids 10 to 22 of SEQ ID NO:84 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 23. Amino acids 14 to 26 of SEQ ID NO:84 are also a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning in this case at amino acid 27. Due to the hydrophobic nature of the predicted leader/signal sequences, each is likely to act as a transmembrane domain should it not be separated from the remainder of the yb186_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yb186_1 should be approximately 2700 bp.

The nucleotide sequence disclosed herein for yb186_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yb186_1 demonstrated at least some similarity with sequences identified as T25270 (Human gene signature HUMGS07432; standard; cDNA to mRNA) and W73738 (zd50d05.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 344073 3', mRNA sequence). Based upon sequence similarity, yb186_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional potential transmembrane domain within the yb186_1 protein sequence centered around amino acid 243 of SEQ ID NO:84.

25

Clone "yb226_1"

A polynucleotide of the present invention has been identified as clone "yb226_1". yb226_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yb226_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yb226_1 protein").

The nucleotide sequence of yb226_1 as presently determined is reported in SEQ ID NO:85, and includes a poly(A) tail. What applicants presently believe to be the proper

reading frame and the predicted amino acid sequence of the yb226_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:86.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yb226_1 should be approximately 1800 bp.

5 The nucleotide sequence disclosed herein for yb226_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yb226_1 demonstrated at least some similarity with sequences identified as N72056 (yv29f11.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone 244173 5', mRNA sequence). Based upon sequence similarity, yb226_1 proteins and
10 each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two potential transmembrane domains within the yb226_1 protein sequence, one around amino acid 54 and another around amino acid 122 of SEQ ID NO:86. Amino acids 45 to 57 and 77 to 89 of SEQ ID NO:86 are also possible leader/signal sequences, with the predicted mature amino acid sequences beginning at amino acids
15 and 90, respectively.

Clone "yd50_1"

A polynucleotide of the present invention has been identified as clone "yd50_1". yd50_1 was isolated from a human adult brain cDNA library and was identified as
20 encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yd50_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yd50_1 protein").

The nucleotide sequence of yd50_1 as presently determined is reported in SEQ ID NO:87, and includes a poly(A) tail. What applicants presently believe to be the proper
25 reading frame and the predicted amino acid sequence of the yd50_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:88.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yd50_1 should be approximately 900 bp.

The nucleotide sequence disclosed herein for yd50_1 was searched against the
30 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yd50_1 demonstrated at least some similarity with sequences identified as AA037761 (zk38c07.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 485100 3', mRNA sequence), AA312218 (EST182969 Jurkat T-cells VI Homo sapiens cDNA 5' end, mRNA sequence), and T24178 (Human gene signature HUMGS06183;

standard; cDNA to mRNA). The predicted amino acid sequence disclosed herein for yd50_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted yd50_1 protein demonstrated at least some similarity to sequences identified as AF038613 (undefined protein [Caenorhabditis elegans]) and AL023286 (hypothetical protein [Schizosaccharomyces pombe]). Based upon sequence similarity, yd50_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the yd50_1 protein sequence centered around amino acid 45 of SEQ ID NO:88.

10

Clone "yd51_1"

A polynucleotide of the present invention has been identified as clone "yd51_1". yd51_1 was isolated from a human adult brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yd51_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yd51_1 protein").

The nucleotide sequence of yd51_1 as presently determined is reported in SEQ ID NO:89, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yd51_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:90. Amino acids 11 to 23 of SEQ ID NO:90 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 24. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yd51_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yd51_1 should be approximately 800 bp.

The nucleotide sequence disclosed herein for yd51_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yd51_1 demonstrated at least some similarity with sequences identified as AA205661 (zq68g09.s1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone 646816 3', mRNA sequence). Based upon sequence similarity, yd51_1 proteins and each similar protein or peptide may share at least some activity.

yd51_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 24 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

5 Clone "yd73_1"

A polynucleotide of the present invention has been identified as clone "yd73_1". yd73_1 was isolated from a human adult brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yd73_1 is a full-length clone, including the
10 entire coding sequence of a secreted protein (also referred to herein as "yd73_1 protein").

The nucleotide sequence of yd73_1 as presently determined is reported in SEQ ID NO:91, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yd73_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:92. Amino
15 acids 67 to 79 of SEQ ID NO:92 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 80. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yd73_1 protein.

20 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yd73_1 should be approximately 1000 bp.

The nucleotide sequence disclosed herein for yd73_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yd73_1 demonstrated at least some similarity with sequences
25 identified as AA587100 (nn81g06.s1 NCI_CGAP_Co9 Homo sapiens cDNA clone IMAGE:1090330, mRNA sequence) and T51192 (Human breast specific gene BSG10 partial cDNA clone HBGDM44; standard; cDNA). The predicted amino acid sequence disclosed herein for yd73_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted yd73_1 protein demonstrated
30 at least some similarity to the sequence identified as AF000198 (No definition line found (T28F2.2) [Caenorhabditis elegans]). Based upon sequence similarity, yd73_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two potential transmembrane domains within the yd73_1 protein

sequence, one centered around amino acid 74 and another around amino acid 169 of SEQ ID NO:92.

yd73_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 23 kDa was detected in membrane fractions using SDS
5 polyacrylamide gel electrophoresis.

Clone "ye43_1"

A polynucleotide of the present invention has been identified as clone "ye43_1". ye43_1 was isolated from a human fetal brain cDNA library and was identified as
10 encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. ye43_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ye43_1 protein").

The nucleotide sequence of ye43_1 as presently determined is reported in SEQ ID NO:93, and includes a poly(A) tail. What applicants presently believe to be the proper
15 reading frame and the predicted amino acid sequence of the ye43_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:94. Amino acids 88 to 100 of SEQ ID NO:94 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 101. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should
20 the predicted leader/signal sequence not be separated from the remainder of the ye43_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ye43_1 should be approximately 1500 bp.

The nucleotide sequence disclosed herein for ye43_1 was searched against the
25 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ye43_1 demonstrated at least some similarity with sequences identified as T23444 (Human gene signature HUMGS05282; standard; cDNA to mRNA) and Z99353 (Homo sapiens mRNA; expressed sequence tag; clone DKFZphamy1_1a12, 3' read, mRNA sequence). Based upon sequence similarity, ye43_1 proteins and each
30 similar protein or peptide may share at least some activity. The TopPredII computer program predicts two potential transmembrane domains within the ye43_1 protein sequence, one centered around amino acid 51 and another around amino acid 89 of SEQ ID NO:94.

Clone "yh71_1"

A polynucleotide of the present invention has been identified as clone "yh71_1".
yh71_1 was isolated from a human brain (fetal and adult) cDNA library and was
identified as encoding a secreted or transmembrane protein on the basis of computer
5 analysis of the amino acid sequence of the encoded protein. yh71_1 is a full-length clone,
including the entire coding sequence of a secreted protein (also referred to herein as
"yh71_1 protein").

The nucleotide sequence of yh71_1 as presently determined is reported in SEQ ID
NO:95, and includes a poly(A) tail. What applicants presently believe to be the proper
10 reading frame and the predicted amino acid sequence of the yh71_1 protein
corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:96. Amino
acids 264 to 276 of SEQ ID NO:96 are a predicted leader/signal sequence, with the
predicted mature amino acid sequence beginning at amino acid 277. Due to the
hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a
15 transmembrane domain should the predicted leader/signal sequence not be separated
from the remainder of the yh71_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone
yh71_1 should be approximately 1891 bp.

The nucleotide sequence disclosed herein for yh71_1 was searched against the
20 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and
FASTA search protocols. yh71_1 demonstrated at least some similarity with sequences
identified as H10493 (y190h09.r1 Homo sapiens cDNA clone 45675 5'), T39809 (Mouse H74
gene; standard; DNA), and X85124 (M.musculus pacsin gene). Based upon sequence
similarity, yh71_1 proteins and each similar protein or peptide may share at least some
25 activity. The TopPredII computer program predicts two additional potential
transmembrane domains within the yh71_1 protein sequence, one centered around amino
acid 122 and another around amino acid 190 of SEQ ID NO:96.

Clone "yh100_1"

30 A polynucleotide of the present invention has been identified as clone "yh100_1".
yh100_1 was isolated from a human brain (fetal and adult) cDNA library and was
identified as encoding a secreted or transmembrane protein on the basis of computer
analysis of the amino acid sequence of the encoded protein. yh100_1 is a full-length clone,

including the entire coding sequence of a secreted protein (also referred to herein as "yh100_1 protein").

The nucleotide sequence of yh100_1 as presently determined is reported in SEQ ID NO:97, and includes a poly(A) tail. What applicants presently believe to be the proper
5 reading frame and the predicted amino acid sequence of the yh100_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:98. Amino acids 35 to 47 of SEQ ID NO:98 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 48. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain
10 should the predicted leader/signal sequence not be separated from the remainder of the yh100_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yh100_1 should be approximately 2200 bp.

The nucleotide sequence disclosed herein for yh100_1 was searched against the
15 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No significant hits were found in the database. The TopPredII computer program predicts an additional potential transmembrane domain within the yh100_1 protein sequence, around amino acid 73 of SEQ ID NO:98. The nucleotide sequence of yh100_1 indicates that it may contain an Alu repetitive element.

20

Clone "yi3_1"

A polynucleotide of the present invention has been identified as clone "yi3_1". yi3_1 was isolated from a human brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid
25 sequence of the encoded protein. yi3_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yi3_1 protein").

The nucleotide sequence of yi3_1 as presently determined is reported in SEQ ID NO:99, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yi3_1 protein corresponding
30 to the foregoing nucleotide sequence is reported in SEQ ID NO:100. Amino acids 20 to 32 of SEQ ID NO:100 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 33. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should

the predicted leader/signal sequence not be separated from the remainder of the yi3_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yi3_1 should be approximately 2000 bp.

5 The nucleotide sequence disclosed herein for yi3_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yi3_1 demonstrated at least some similarity with sequences identified as N22677 (yx64a05.s1 Homo sapiens cDNA clone 266480 3'). Based upon sequence similarity, yi3_1 proteins and each similar protein or peptide may share at least
10 some activity.

Clone "yj23_1"

A polynucleotide of the present invention has been identified as clone "yj23_1". yj23_1 was isolated from a human fetal kidney (293 cell line) cDNA library and was
15 identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yj23_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yj23_1 protein").

The nucleotide sequence of yj23_1 as presently determined is reported in SEQ ID
20 NO:101, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yj23_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:102. Amino acids 12 to 24 of SEQ ID NO:102 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 25. Amino acids 15 to 27 of SEQ ID NO:102
25 are also a possible leader/signal sequence, with the predicted mature amino acid sequence beginning in this case at amino acid 28, or are a transmembrane domain. Due to the hydrophobic nature of the predicted leader/signal sequences, each is likely to act as a transmembrane domain should it not be separated from the remainder of the yj23_1 protein.

30 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yj23_1 should be approximately 1400 bp.

The nucleotide sequence disclosed herein for yj23_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yj23_1 demonstrated at least some similarity with sequences

identified as AI096483 (qa03c12.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:1685686 3' similar to TR:Q04386 Q04386 HYPOTHETICAL 29.1 KD PROTEIN IN RPII140 5'REGION; mRNA sequence) and T19036 (Human gene signature HUMGS00043; standard; cDNA to mRNA). Based upon sequence similarity, yj23_1 proteins and each
5 similar protein or peptide may share at least some activity. The TopPredII computer program predicts two additional potential transmembrane domains within the yj23_1 protein sequence, one centered around amino acid 90 and another around amino acid 199 of SEQ ID NO:102.

10 Clone "yl9_1"

A polynucleotide of the present invention has been identified as clone "yl9_1". yl9_1 was isolated from a human adult spleen cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yl9_1 is a full-length clone, including the
15 entire coding sequence of a secreted protein (also referred to herein as "yl9_1 protein").

The nucleotide sequence of yl9_1 as presently determined is reported in SEQ ID NO:103, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yl9_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:104. Amino acids 6 to 18
20 of SEQ ID NO:104 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 19. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yl9_1 protein.

25 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yl9_1 should be approximately 1100 bp.

The nucleotide sequence disclosed herein for yl9_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yl9_1 demonstrated at least some similarity with sequences
30 identified as AA902287 (ok69g10.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE 1519266 3' similar to SW C1QA_HUMAN P02745 COMPLEMENT C1Q SUB-COMPONENT, A CHAIN PRECURSOR; mRNA sequence) and X58861 (Mouse mRNA for complement subcomponent C1Q alpha-chain). The predicted amino acid sequence disclosed herein for yl9_1 was searched against the GenPept and GeneSeq amino acid

sequence databases using the BLASTX search protocol. The predicted yl9_1 protein demonstrated at least some similarity to sequences identified as R22265 (New collagen type protein from chipmunk blood), W09108 (Human adipocyte complement related protein Acrp30), and X58861 (complement subcomponent C1Q A-chain precursor [Mus musculus]). Based upon sequence similarity, yl9_1 proteins and each similar protein or peptide may share at least some activity. The predicted yl9_1 protein has at least some similarity to human, mouse, and rat complement subcomponent C1Q, and motifs and profile hidden markov model analysis of the predicted yl9_1 protein have revealed the presence of a C1Q domain signature at amino acids 116 to 241 of SEQ ID NO:104. C1Q is a subunit of the C1 enzyme complex that activates the serum complement system. The collagen-like regions of C1Q interact with the Ca(2+)-Dependent C1R(2)/C1S(2) proenzyme complex, and efficient activation of C1 takes place on interaction of the globular heads of C1Q with the Fc regions of IgG or IgM antibody present in immune complexes. The C1Q domain has been found in the C-terminus of vertebrate secreted or membrane-bound proteins which are mostly short-chain collagens and collagen-like molecules. The predicted yl9_1 protein appears to encode a novel member of the C1 enzyme complex, having the highest degree of similarity to the A-chain of the complex. The TopPredII computer program predicts a potential transmembrane domain within the yl9_1 protein sequence centered around amino acid 160 of SEQ ID NO:104.

yl9_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 23 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "ya66_1"

A polynucleotide of the present invention has been identified as clone "ya66_1". ya66_1 was isolated from a human adult testes cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. ya66_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ya66_1 protein").

The nucleotide sequence of ya66_1 as presently determined is reported in SEQ ID NO:105, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the ya66_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:106.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ya66_1 should be approximately 1050 bp.

The nucleotide sequence disclosed herein for ya66_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ya66_1 demonstrated at least some similarity with sequences identified as AI096636 (qb57c12.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:1704214 3', mRNA sequence) and T20099 (Human gene signature HUMGS01242; standard; cDNA to mRNA). Based upon sequence similarity, ya66_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the ya66_1 protein sequence centered around amino acid 106 of SEQ ID NO:106.

Clone "yb187_1"

A polynucleotide of the present invention has been identified as clone "yb187_1". yb187_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yb187_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yb187_1 protein").

The nucleotide sequence of yb187_1 as presently determined is reported in SEQ ID NO:107, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yb187_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:108.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yb187_1 should be approximately 1800 bp.

The nucleotide sequence disclosed herein for yb187_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yb187_1 demonstrated at least some similarity with sequences identified as AA846805 (aj99f04.s1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone IMAGE:1404607 3', mRNA sequence) and Q61039 (Human brain Expressed Sequence Tag EST01102; standard; DNA). Based upon sequence similarity, yb187_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the yb187_1 protein sequence centered around amino acid 58 of SEQ ID NO:108; amino acids

58 to 70 of SEQ ID NO:108 are also a possible leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 71.

Clone "yb219_1"

5 A polynucleotide of the present invention has been identified as clone "yb219_1". yb219_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yb219_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yb219_1 protein").

10 The nucleotide sequence of yb219_1 as presently determined is reported in SEQ ID NO:109, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yb219_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:110. Amino acids 3 to 15 of SEQ ID NO:110 are a predicted leader/signal sequence, with the
15 predicted mature amino acid sequence beginning at amino acid 16. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yb219_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone
20 yb219_1 should be approximately 1600 bp.

The nucleotide sequence disclosed herein for yb219_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No significant hits were found in the database.

25 Clone "yb228_1"

A polynucleotide of the present invention has been identified as clone "yb228_1". yb228_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yb228_1 is a full-length clone, including the
30 entire coding sequence of a secreted protein (also referred to herein as "yb228_1 protein").

The nucleotide sequence of yb228_1 as presently determined is reported in SEQ ID NO:111, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yb228_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:112.

Amino acids 1 to 13 of SEQ ID NO:112 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 14. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated
5 from the remainder of the yb228_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yb228_1 should be approximately 650 bp.

The nucleotide sequence disclosed herein for yb228_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and
10 FASTA search protocols. No hits were found in the database. The TopPredII computer program predicts a potential transmembrane domain within the yb228_1 protein sequence centered around amino acid 31 of SEQ ID NO:112.

Clone "yc27_1"

15 A polynucleotide of the present invention has been identified as clone "yc27_1". yc27_1 was isolated from a human fetal kidney (293 embryonal carcinoma cell line) cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yc27_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to
20 herein as "yc27_1 protein").

The nucleotide sequence of yc27_1 as presently determined is reported in SEQ ID NO:113, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yc27_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:114. Amino acids 111 to
25 123 of SEQ ID NO:114 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 124. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yc27_1 protein.

30 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yc27_1 should be approximately 1300 bp.

The nucleotide sequence disclosed herein for yc27_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yc27_1 demonstrated at least some similarity with sequences

identified as T23290 (Human gene signature HUMGS05104; standard; cDNA to mRNA) and W60958 (zc98d11.s1 Pancreatic Islet Homo sapiens cDNA clone 339189 3', mRNA sequence). The predicted amino acid sequence disclosed herein for yc27_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted yc27_1 protein demonstrated at least some similarity to sequences identified as AL021890 (undefined protein [Arabidopsis thaliana]) and U00036 (R151.6 [Caenorhabditis elegans]). Based upon sequence similarity, yc27_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts three potential transmembrane domains within the yc27_1 protein sequence, centered around amino acids 68, 107, and 161 of SEQ ID NO:114, respectively.

yc27_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 23 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

15 Clone "yc49_1"

A polynucleotide of the present invention has been identified as clone "yc49_1". yc49_1 was isolated from a human fetal kidney (293 embryonal carcinoma cell line) cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yc49_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yc49_1 protein").

The nucleotide sequence of yc49_1 as presently determined is reported in SEQ ID NO:115, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yc49_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:116.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yc49_1 should be approximately 1000 bp.

The nucleotide sequence disclosed herein for yc49_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yc49_1 demonstrated at least some similarity with sequences identified as AF052113 (Homo sapiens clone 23675 mRNA sequence), N28761 (yx69b12.r1 Homo sapiens cDNA clone 266975 5'), and T20571 (Human gene signature HUMGS01786; standard; cDNA to mRNA). Based upon sequence similarity, yc49_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer

program predicts two potential transmembrane domains within the yc49_1 protein sequence, one centered around amino acid 48 and another around amino acid 75 of SEQ ID NO:116. Amino acids 38 to 50 of SEQ ID NO:116 are also a possible leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 51.

5

Clone "yd40_1"

A polynucleotide of the present invention has been identified as clone "yd40_1". yd40_1 was isolated from a human adult brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yd40_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yd40_1 protein").

The nucleotide sequence of yd40_1 as presently determined is reported in SEQ ID NO:117, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yd40_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:118.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yd40_1 should be approximately 900 bp.

The nucleotide sequence disclosed herein for yd40_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No significant hits were found in the database. The TopPredII computer program predicts three potential transmembrane domains within the yd40_1 protein sequence, centered around amino acids 19, 60, and 86 of SEQ ID NO:118, respectively. The nucleotide sequence of yd40_1 indicates that it may contain a MIR repetitive element.

25

Clone "yd64_1"

A polynucleotide of the present invention has been identified as clone "yd64_1". yd64_1 was isolated from a human adult brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yd64_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yd64_1 protein").

The nucleotide sequence of yd64_1 as presently determined is reported in SEQ ID NO:119, and includes a poly(A) tail. What applicants presently believe to be the proper

reading frame and the predicted amino acid sequence of the yd64_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:120.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yd64_1 should be approximately 1000 bp.

5 The nucleotide sequence disclosed herein for yd64_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yd64_1 demonstrated at least some similarity with sequences identified as N59133 (yz62c12.s1 Soares multiple sclerosis 2NbHMSP Homo sapiens cDNA clone 287638 3', mRNA sequence). The predicted amino acid sequence disclosed
10 herein for yd64_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted yd64_1 protein demonstrated at least some similarity to sequences identified as M98529 (21 kDa protein [Homo sapiens]). Based upon sequence similarity, yd64_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a
15 potential transmembrane domains within the yd64_1 protein sequence centered around amino acid 96 of SEQ ID NO:120.

 yd64_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 23 kDa was detected in conditioned medium using SDS polyacrylamide gel electrophoresis.

20

Clone "ye47_1"

 A polynucleotide of the present invention has been identified as clone "ye47_1". ye47_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the
25 amino acid sequence of the encoded protein. ye47_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ye47_1 protein").

 The nucleotide sequence of ye47_1 as presently determined is reported in SEQ ID NO:121, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the ye47_1 protein corresponding
30 to the foregoing nucleotide sequence is reported in SEQ ID NO:122. Amino acids 40 to 52 of SEQ ID NO:122 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 53. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should

the predicted leader/signal sequence not be separated from the remainder of the ye47_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ye47_1 should be approximately 1600 bp.

5 The nucleotide sequence disclosed herein for ye47_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ye47_1 demonstrated at least some similarity with sequences identified as AC000105 (** SEQUENCING IN PROGRESS ** Homo sapiens Chromosome 22q11.2 MDR Region; HTGS phase 2, 6 ordered pieces). Based upon
10 sequence similarity, ye47_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional potential transmembrane domain within the ye47_1 protein sequence centered around amino acid 42 of SEQ ID NO:122. The nucleotide sequence of ye47_1 indicates that it may contain one or more of the following repetitive elements: Alu, MIR.

15 ye47_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 24 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "yh50_1"

20 A polynucleotide of the present invention has been identified as clone "yh50_1". yh50_1 was isolated from a human brain (fetal and adult) cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yh50_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as
25 "yh50_1 protein").

 The nucleotide sequence of yh50_1 as presently determined is reported in SEQ ID NO:123, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yh50_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:124.
30 Amino acids 35 to 47 of SEQ ID NO:124 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 48. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yh50_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yh50_1 should be approximately 2515 bp.

The nucleotide sequence disclosed herein for yh50_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yh50_1 demonstrated at least some similarity with sequences identified as N49425 (yv21c11.r1 Homo sapiens cDNA clone 243380 5' similar to contains Alu repetitive element), Q90512 (CEA clone HindIII-Sau3A fragment; standard; DNA), and R98218 (yq75a05.r1 Homo sapiens cDNA clone 201584 5' similar to contains Alu repetitive element). Based upon sequence similarity, yh50_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of yh50_1 indicates that it may contain an Alu repetitive element.

Clone "yh53_1"

A polynucleotide of the present invention has been identified as clone "yh53_1". yh53_1 was isolated from a human brain (fetal and adult) cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yh53_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yh53_1 protein").

The nucleotide sequence of yh53_1 as presently determined is reported in SEQ ID NO:125, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yh53_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:126.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yh53_1 should be approximately 1763 bp.

The nucleotide sequence disclosed herein for yh53_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yh53_1 demonstrated at least some similarity with sequences identified as T23683 (Human gene signature HUMGS05558; standard; cDNA to mRNA) and W52762 (zd13a08.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 340502 5', mRNA sequence). Based upon sequence similarity, yh53_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the yh53_1 protein sequence centered around amino acid 23 of SEQ ID NO:126.

Clone "yh98_1"

A polynucleotide of the present invention has been identified as clone "yh98_1".
yh98_1 was isolated from a human brain (fetal and adult) cDNA library and was
identified as encoding a secreted or transmembrane protein on the basis of computer
5 analysis of the amino acid sequence of the encoded protein. yh98_1 is a full-length clone,
including the entire coding sequence of a secreted protein (also referred to herein as
"yh98_1 protein").

The nucleotide sequence of yh98_1 as presently determined is reported in SEQ ID
NO:127, and includes a poly(A) tail. What applicants presently believe to be the proper
10 reading frame and the predicted amino acid sequence of the yh98_1 protein
corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:128.
Amino acids 24 to 36 of SEQ ID NO:128 are a predicted leader/signal sequence, with the
predicted mature amino acid sequence beginning at amino acid 37. Due to the
hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a
15 transmembrane domain should the predicted leader/signal sequence not be separated
from the remainder of the yh98_1 protein.

Another potential yh98_1 reading frame and predicted amino acid sequence that
could be encoded by basepairs 1381 to 1635 of SEQ ID NO:127 is reported in SEQ ID
NO:266. Amino acids 64 to 76 of SEQ ID NO:266 are a predicted leader/signal sequence,
20 with the predicted mature amino acid sequence beginning at amino acid 77. Due to the
hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a
transmembrane domain should the predicted leader/signal sequence not be separated
from the remainder of the protein of SEQ ID NO:266.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone
25 yh98_1 should be approximately 1000 bp.

The nucleotide sequence disclosed herein for yh98_1 was searched against the
GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and
FASTA search protocols. yh98_1 demonstrated at least some similarity with sequences
identified as AA187630 (zp73e04.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA
30 clone 625854 3', mRNA sequence), AA632023 (np74d10.s1 NCI_CGAP_Br2 Homo sapiens
cDNA clone IMAGE:1132051, mRNA sequence), AA837470 (od20e11.s1
NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1368524, mRNA sequence),
AF034176 (Homo sapiens ntcon5 contig mRNA, partial sequence, mRNA sequence),
AF052101 (Homo sapiens clone 23872 mRNA sequence), AI092946 (qa81c03.x1

Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1693156 3', mRNA sequence), and Q76621 (Human genome fragment (Preferred); standard; DNA). Based upon sequence similarity, yh98_1 proteins and each similar protein or peptide may share at least some activity.

5

Clone "ya69_1"

A polynucleotide of the present invention has been identified as clone "ya69_1". ya69_1 was isolated from a human adult testes cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. ya69_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ya69_1 protein").

The nucleotide sequence of ya69_1 as presently determined is reported in SEQ ID NO:129, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the ya69_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:130. Amino acids 35 to 47 of SEQ ID NO:130 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 48. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the ya69_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ya69_1 should be approximately 2000 bp.

The nucleotide sequence disclosed herein for ya69_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ya69_1 demonstrated at least some similarity with sequences identified as AI075196 (oy96c08.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1673678 3', mRNA sequence). Based upon sequence similarity, ya69_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the ya69_1 protein sequence, centered around amino acid 40 of SEQ ID NO:130.

Clone "yd107_1"

A polynucleotide of the present invention has been identified as clone "yd107_1". yd107_1 was isolated from a human adult brain cDNA library and was identified as

encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yd107_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yd107_1 protein").

The nucleotide sequence of yd107_1 as presently determined is reported in SEQ ID NO:131, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yd107_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:132. Amino acids 37 to 49 of SEQ ID NO:132 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 50. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yd107_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yd107_1 should be approximately 1000 bp.

The nucleotide sequence disclosed herein for yd107_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yd107_1 demonstrated at least some similarity with sequences identified as AA910935 (ok85f02.s1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1520763 3' similar to WP:R05D11.5 CE06240; mRNA sequence) and T26576 (Human gene signature HUMGS08822; standard; cDNA to mRNA). The predicted amino acid sequence disclosed herein for yd107_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted yd107_1 protein demonstrated at least some similarity to sequences identified as Z75546 (R05D11.5 [Caenorhabditis elegans]). Based upon sequence similarity, yd107_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two potential transmembrane domains within the yd107_1 protein sequence, one centered around amino acid 48 and another around amino acid 121 of SEQ ID NO:132.

Clone "yd145_1"

A polynucleotide of the present invention has been identified as clone "yd145_1". yd145_1 was isolated from a human adult brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the

amino acid sequence of the encoded protein. yd145_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yd145_1 protein").

The nucleotide sequence of yd145_1 as presently determined is reported in SEQ ID NO:133, and includes a poly(A) tail. What applicants presently believe to be the proper
5 reading frame and the predicted amino acid sequence of the yd145_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:134. Amino acids 3 to 15 of SEQ ID NO:134 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 16. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a
10 transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yd145_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yd145_1 should be approximately 750 bp.

The nucleotide sequence disclosed herein for yd145_1 was searched against the
15 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yd145_1 demonstrated at least some similarity with sequences identified as AA432034 (zw80e01.r1 Soares testis NHT Homo sapiens cDNA clone 782520 5', mRNA sequence) and X87489 (H.sapiens genomic DNA (chromosome 3; clone NL1243D)). Based upon sequence similarity, yd145_1 proteins and each similar protein
20 or peptide may share at least some activity. The TopPredII computer program predicts an additional potential transmembrane domain within the yd145_1 protein sequence centered around amino acid 45 of SEQ ID NO:134:

Clone "yh24_1"

25 A polynucleotide of the present invention has been identified as clone "yh24_1". yh24_1 was isolated from a human brain (fetal and adult) cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yh24_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as
30 "yh24_1 protein").

The nucleotide sequence of yh24_1 as presently determined is reported in SEQ ID NO:135, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yh24_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:136.

Another potential yh24_1 reading frame and predicted amino acid sequence that could be encoded by basepairs 676 to 939 of SEQ ID NO:135 is reported in SEQ ID NO:267.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yh24_1 should be approximately 1000 bp.

5 The nucleotide sequence disclosed herein for yh24_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yh24_1 demonstrated at least some similarity with sequences identified as AA129061 (zo11f12.r1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone 567407 5' similar to TR:G439877 G439877 REVERSE TRAN-
10 SCRIPTASE; mRNA sequence). Based upon sequence similarity, yh24_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two potential transmembrane domains within the yh24_1 protein sequence of SEQ ID NO:136, one centered around amino acid 52 and another near the N-terminus of SEQ ID NO:136, the latter domain also being a possible signal/leader
15 sequence. Analysis of the possible yh24_1 amino acid sequence of SEQ ID NO:267 reveals a binding-protein-dependent transport systems inner membrane component signature. This signature is present in the integral inner-membrane proteins superfamily which translocate substrates across the membrane.

20 Clone "yi11_1"

A polynucleotide of the present invention has been identified as clone "yi11_1". yi11_1 was isolated from a human brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yi11_1 is a full-length clone, including the entire coding
25 sequence of a secreted protein (also referred to herein as "yi11_1 protein").

The nucleotide sequence of yi11_1 as presently determined is reported in SEQ ID NO:137, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yi11_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:138. Amino acids 128 to
30 140 of SEQ ID NO:138 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 141. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yi11_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yi11_1 should be approximately 1550 bp.

The nucleotide sequence disclosed herein for yi11_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yi11_1 demonstrated at least some similarity with sequences identified as AA772340 (ai43c02.s1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 1359746 3', mRNA sequence), T26648 (Human gene signature HUMGS08895; standard; cDNA to mRNA), and U48972 (Mus musculus spindlin (Spin) mRNA, complete cds). Based upon sequence similarity, yi11_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts four potential transmembrane domains within the yi11_1 protein sequence, centered around amino acids 20, 45, 90, and 136 of SEQ ID NO:138, respectively, with the most N-terminal domain also being a possible signal/leader sequence.

15 Clone "yi18_1".

A polynucleotide of the present invention has been identified as clone "yi18_1". yi18_1 was isolated from a human brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yi18_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yi18_1 protein").

The nucleotide sequence of yi18_1 as presently determined is reported in SEQ ID NO:139, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yi18_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:140. Amino acids 48 to 60 of SEQ ID NO:140 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 61. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yi18_1 protein.

30 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yi18_1 should be approximately 1850 bp.

The nucleotide sequence disclosed herein for yi18_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yi18_1 demonstrated at least some similarity with sequences

identified as AC003086 Human BAC clone RG104F04 from 7q21-q22, complete sequence), T81349 (yd27c10.s1 Homo sapiens cDNA clone 109458 3'), and T81524 (yd27c10.r1 Homo sapiens cDNA clone 109458 5'). Based upon sequence similarity, yk18_1 proteins and each similar protein or peptide may share at least some activity.

5

Clone "yk14_1"

A polynucleotide of the present invention has been identified as clone "yk14_1". yk14_1 was isolated from a human adult thymus cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yk14_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yk14_1 protein").

The nucleotide sequence of yk14_1 as presently determined is reported in SEQ ID NO:141, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yk14_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:142. Amino acids 17 to 29 of SEQ ID NO:142 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 30. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yk14_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yk14_1 should be approximately 1067 bp.

The nucleotide sequence disclosed herein for yk14_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yk14_1 demonstrated at least some similarity with sequences identified as AA576618 (nm74f07.s1 NCI_CGAP_Co9 Homo sapiens cDNA clone IMAGE:1073989, mRNA sequence). Based upon sequence similarity, yk14_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional potential transmembrane domains within the yk14_1 protein sequence centered around amino acid 61 of SEQ ID NO:142.

Clone "yk39_1"

A polynucleotide of the present invention has been identified as clone "yk39_1". yk39_1 was isolated from a human adult thymus cDNA library and was identified as

encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yk39_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yk39_1 protein").

5 The nucleotide sequence of yk39_1 as presently determined is reported in SEQ ID NO:143, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yk39_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:144.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yk39_1 should be approximately 1300 bp.

10 The nucleotide sequence disclosed herein for yk39_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No significant hits were found in the database. The TopPredII computer program predicts two potential transmembrane domains within the yk39_1 protein sequence, one centered around amino acid 18 and another around amino acid 44
15 of SEQ ID NO:144. The nucleotide sequence of yk39_1 indicates that it may contain a MIR repeat region.

Clone "yk91_1"

A polynucleotide of the present invention has been identified as clone "yk91_1".

20 yk91_1 was isolated from a human adult thymus cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yk91_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yk91_1 protein").

The nucleotide sequence of yk91_1 as presently determined is reported in SEQ ID
25 NO:145, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yk91_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:146. Amino acids 49 to 61 of SEQ ID NO:146 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 62. Due to the
30 hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yk91_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yk91_1 should be approximately 1150 bp.

The nucleotide sequence disclosed herein for yk91_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No significant hits were found in the database. The TopPredII computer program predicts an additional potential transmembrane domain within the yk91_1 protein sequence centered around amino acid 80 of SEQ ID NO:146. The nucleotide sequence of yk91_1 indicates that it may contain an Alu repetitive element.

Clone "yk199_1"

A polynucleotide of the present invention has been identified as clone "yk199_1". yk199_1 was isolated from a human adult thymus cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yk199_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yk199_1 protein").

The nucleotide sequence of yk199_1 as presently determined is reported in SEQ ID NO:147, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yk199_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:148. Amino acids 10 to 22 of SEQ ID NO:148 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 23. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yk199_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yk199_1 should be approximately 1700 bp.

The nucleotide sequence disclosed herein for yk199_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yk199_1 demonstrated at least some similarity with sequences identified as AI039293 (ox33e12.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1658158 3', mRNA sequence). Based upon sequence similarity, yk199_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the yk199_1 protein sequence, around amino acid 132 of SEQ ID NO:148. The nucleotide sequence and the predicted amino acid sequence of yk199_1 indicate that it may contain human TAR1 (telomere-associated repeat 1) sequence.

Clone "yl4_1"

A polynucleotide of the present invention has been identified as clone "yl4_1". yl4_1 was isolated from a human adult spleen cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yl4_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yl4_1 protein").

The nucleotide sequence of yl4_1 as presently determined is reported in SEQ ID NO:149, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yl4_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:150. Amino acids 204 to 216 of SEQ ID NO:150 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 217. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yl4_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yl4_1 should be approximately 1250 bp.

The nucleotide sequence disclosed herein for yl4_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yl4_1 demonstrated at least some similarity with sequences identified as AA283813 (zt19g10.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 713634 3', mRNA sequence). Based upon sequence similarity, yl4_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional potential transmembrane domain within the yl4_1 protein sequence centered around amino acid 108 of SEQ ID NO:150.

Clone "yl14_1"

A polynucleotide of the present invention has been identified as clone "yl14_1". yl14_1 was isolated from a human adult spleen cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yl14_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yl14_1 protein").

The nucleotide sequence of yl14_1 as presently determined is reported in SEQ ID NO:151, and includes a poly(A) tail. What applicants presently believe to be the proper

reading frame and the predicted amino acid sequence of the yl14_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:152.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yl14_1 should be approximately 1000 bp.

- 5 The nucleotide sequence disclosed herein for yl14_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yl14_1 demonstrated at least some similarity with sequences identified as AF034174 (Homo sapiens ntcon3 contig mRNA, partial sequence, mRNA sequence) and T03943 (human thrombopoietin genomic coding sequence). Based upon
10 sequence similarity, yl14_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two potential transmembrane domains within the yl14_1 protein sequence, one centered around amino acid 18 and another around amino acid 69 of SEQ ID NO:152; amino acids 61 to 73 are also a possible leader/signal sequence, with the predicted mature amino acid sequence beginning at
15 amino acid 74 of SEQ ID NO:152. The nucleotide sequence of yl14_1 indicates that it may contain an Alu repetitive element.

Clone "ya80_1"

- A polynucleotide of the present invention has been identified as clone "ya80_1".
20 ya80_1 was isolated from a human adult testes cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. ya80_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ya80_1 protein").

- The nucleotide sequence of ya80_1 as presently determined is reported in SEQ ID
25 NO:153, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the ya80_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:154. Amino acids 31 to 43 of SEQ ID NO:154 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 44. Due to the hydrophobic nature of the
30 predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the ya80_1 protein.

 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ya80_1 should be approximately 600 bp.

The nucleotide sequence disclosed herein for ya80_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No significant hits were found in the database. The TopPredII computer program predicts a potential transmembrane domain within the ya80_1 protein
5 sequence centered around amino acid 30 of SEQ ID NO:154.

Clone "yd61_1"

A polynucleotide of the present invention has been identified as clone "yd61_1". yd61_1 was isolated from a human adult brain cDNA library and was identified as
10 encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yd61_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yd61_1 protein").

The nucleotide sequence of yd61_1 as presently determined is reported in SEQ ID NO:155, and includes a poly(A) tail. What applicants presently believe to be the proper
15 reading frame and the predicted amino acid sequence of the yd61_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:156. Amino acids 156 to 168 of SEQ ID NO:156 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 169. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a
20 transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yd61_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yd61_1 should be approximately 950 bp.

The nucleotide sequence disclosed herein for yd61_1 was searched against the
25 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yd61_1 demonstrated at least some similarity with sequences identified as AI017161 (ou28a07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627572 3' similar to TR:Q15040 Q15040 MRNA ;contains TAR1.t1 MSR1 repetitive element; mRNA sequence) and D31884 (Human mRNA for KIAA0063 gene,
30 complete cds). The predicted amino acid sequence disclosed herein for yd61_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted yd61_1 protein demonstrated at least some similarity to the sequence identified as D31884 (KIAA0063 [Homo sapiens]). Based upon sequence similarity, yd61_1 proteins and each similar protein or peptide may share at

least some activity. The TopPredII computer program predicts two potential transmembrane domains within the yd61_1 protein sequence, one centered around amino acid 78 and another around amino acid 11 of SEQ ID NO:156.

5 Clone "yd88_1"

A polynucleotide of the present invention has been identified as clone "yd88_1". yd88_1 was isolated from a human adult brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yd88_1 is a full-length clone, including the
10 entire coding sequence of a secreted protein (also referred to herein as "yd88_1 protein").

The nucleotide sequence of yd88_1 as presently determined is reported in SEQ ID NO:157, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yd88_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:158.

15 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yd88_1 should be approximately 1000 bp.

The nucleotide sequence disclosed herein for yd88_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yd88_1 demonstrated at least some similarity with sequences
20 identified as W22362 (66B4 Human retina cDNA Tsp509I-cleaved sublibrary Homo sapiens cDNA not directional, mRNA sequence). Based upon sequence similarity, yd88_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domains within the yd88_1 protein sequence, around amino acid 60 of SEQ ID NO:158.

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Clone "yd109_1"

A polynucleotide of the present invention has been identified as clone "yd109_1". yd109_1 was isolated from a human adult brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the
30 amino acid sequence of the encoded protein. yd109_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yd109_1 protein").

The nucleotide sequence of yd109_1 as presently determined is reported in SEQ ID NO:159, and includes a poly(A) tail. What applicants presently believe to be the proper

reading frame and the predicted amino acid sequence of the yd109_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:160.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yd109_1 should be approximately 550 bp.

5 The nucleotide sequence disclosed herein for yd109_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yd109_1 demonstrated at least some similarity with sequences identified as AA809139 (nw17h06.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1240763, mRNA sequence) and T21990 (Human gene signature HUMGS03533; standard; cDNA to mRNA). The predicted amino acid sequence disclosed herein for yd109_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted yd109_1 protein demonstrated at least some similarity to the sequence identified as U80438 (coded for by C. elegans cDNA CEESD64F; similar to a short region of DNAJ proteins in part of the DNAJ-like domain
10 [Caenorhabditis elegans]). Based upon sequence similarity, yd109_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the yd109_1 protein sequence, centered around a position between amino acid 50 and amino acid 54 of SEQ ID NO:160.
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Clone "yd141_1"

A polynucleotide of the present invention has been identified as clone "yd141_1". yd141_1 was isolated from a human adult brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the
25 amino acid sequence of the encoded protein. yd141_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yd141_1 protein").

The nucleotide sequence of yd141_1 as presently determined is reported in SEQ ID NO:161, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yd141_1 protein
30 corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:162.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yd141_1 should be approximately 650 bp.

The nucleotide sequence disclosed herein for yd141_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and

FASTA search protocols. yd141_1 demonstrated at least some similarity with sequences identified as AA974564 (op28f05.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE 1578177 3', mRNA sequence) and AC004789 (Homo sapiens chromosome 16, cosmid clone RT140 (LANL), complete sequence). Based upon sequence similarity, yd141_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts six potential transmembrane domains within the yd141_1 protein sequence, one centered around amino acid 46 and others around amino acids 10, 35, 70, 93 and 100 of SEQ ID NO:162, respectively.

yd141_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 13 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "yd153_1"

A polynucleotide of the present invention has been identified as clone "yd153_1". yd153_1 was isolated from a human adult brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yd153_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yd153_1 protein").

The nucleotide sequence of yd153_1 as presently determined is reported in SEQ ID NO:163, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yd153_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:164. Amino acids 18 to 30 of SEQ ID NO:164 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 31. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yd153_1 protein.

Another potential yd153_1 reading frame and predicted amino acid sequence is encoded by basepairs 68 to 244 of SEQ ID NO:163 and is reported in SEQ ID NO:268.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yd153_1 should be approximately 650 bp.

The nucleotide sequence disclosed herein for yd153_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yd153_1 demonstrated at least some similarity with sequences

identified as AA309873 (EST180736 Jurkat T-cells V Homo sapiens cDNA 5' end, mRNA sequence) and T26022 (Human gene signature HUMGS08258; standard; cDNA to mRNA). Based upon sequence similarity, yd153_1 proteins and each similar protein or peptide may share at least some activity.

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Clone "yd165_1"

A polynucleotide of the present invention has been identified as clone "yd165_1". yd165_1 was isolated from a human adult brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yd165_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yd165_1 protein").

The nucleotide sequence of yd165_1 as presently determined is reported in SEQ ID NO:165, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yd165_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:166.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yd165_1 should be approximately 650 bp.

The nucleotide sequence disclosed herein for yd165_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yd165_1 demonstrated at least some similarity with sequences identified as AA873304 (oh75h10.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE 1472899 3' similar to SW INI7_HUMAN P40305 INTERFERON-ALPHA INDUCED 11.5 KD PROTEIN; mRNA sequence), V24016 (Human interferon-inducible protein, HIFI, coding sequence; standard; cDNA), and X67325 (H.sapiens p27 mRNA). The predicted amino acid sequence disclosed herein for yd165_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted yd165_1 protein demonstrated at least some similarity to sequences identified as U22970 (interferon-inducible peptide precursor [Homo sapiens]), W54040 (Human interferon-inducible protein, HIFI), and X67325 (p27 gene product [Homo sapiens]). Based upon sequence similarity, yd165_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts three potential transmembrane domains within the yd165_1 protein sequence, centered around amino acids 43, 77, and 107 of SEQ ID NO:166, respectively.

Clone "yd178_1"

A polynucleotide of the present invention has been identified as clone "yd178_1". yd178_1 was isolated from a human adult brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yd178_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yd178_1 protein").

The nucleotide sequence of yd178_1 as presently determined is reported in SEQ ID NO:167, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yd178_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:168. Amino acids 7 to 19 of SEQ ID NO:168 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 20. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yd178_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yd178_1 should be approximately 900 bp.

The nucleotide sequence disclosed herein for yd178_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yd178_1 demonstrated at least some similarity with sequences identified as AI141062 (oz43g12.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1678150 3' similar to SW:LYG_ANSAN P00718 LYSOZYME G; mRNA sequence) and X61002 (G.gallus mRNA for goose-type lysozyme). The predicted amino acid sequence disclosed herein for yd178_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted yd178_1 protein demonstrated at least some similarity to the sequence identified as X61002 (lysozyme [Gallus gallus]), and chicken "goose-type" lysozymes. Based upon sequence similarity, yd178_1 proteins and each similar protein or peptide may share at least some activity.

yd178_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 23 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "yd191_1"

A polynucleotide of the present invention has been identified as clone "yd191_1". yd191_1 was isolated from a human adult brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yd191_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yd191_1 protein").

The nucleotide sequence of yd191_1 as presently determined is reported in SEQ ID NO:169, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yd191_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:170.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yd191_1 should be approximately 550 bp.

The nucleotide sequence disclosed herein for yd191_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yd191_1 demonstrated at least some similarity with sequences identified as H98768 (yx13d09.s1 Homo sapiens cDNA clone 261617 3'). Based upon sequence similarity, yd191_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two potential transmembrane domains within the yd191_1 protein sequence, one centered around amino acid 55 and another around amino acid 68 of SEQ ID NO:170.

Clone "ye7_1"

A polynucleotide of the present invention has been identified as clone "ye7_1". ye7_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. ye7_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ye7_1 protein").

The nucleotide sequence of ye7_1 as presently determined is reported in SEQ ID NO:171, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the ye7_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:172.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ye7_1 should be approximately 2400 bp.

The nucleotide sequence disclosed herein for ye7_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ye7_1 demonstrated at least some similarity with sequences identified as AI017060 (ov01d06.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone
5 IMAGE:1636043 3', mRNA sequence). Based upon sequence similarity, ye7_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two potential transmembrane domains within the ye7_1 protein sequence, one centered around amino acid 65 and another around amino acid 105 of SEQ ID NO:172.

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Clone "yf33_1"

A polynucleotide of the present invention has been identified as clone "yf33_1". yf33_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the
15 amino acid sequence of the encoded protein. yf33_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yf33_1 protein").

The nucleotide sequence of yf33_1 as presently determined is reported in SEQ ID NO:173, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yf33_1 protein corresponding
20 to the foregoing nucleotide sequence is reported in SEQ ID NO:174. Amino acids 36 to 48 of SEQ ID NO:174 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 49. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yf33_1
25 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yf33_1 should be approximately 2500 bp.

The nucleotide sequence disclosed herein for yf33_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and
30 FASTA search protocols. No significant hits were found in the database. The TopPredII computer program predicts a potential transmembrane domain within the yf33_1 protein sequence centered around amino acids 93 of SEQ ID NO:174. The nucleotide sequence of yf33_1 indicates that it may contain an Alu repetitive element.

Clone "yi15_1"

A polynucleotide of the present invention has been identified as clone "yi15_1". yi15_1 was isolated from a human brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yi15_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yi15_1 protein").

The nucleotide sequence of yi15_1 as presently determined is reported in SEQ ID NO:175, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yi15_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:176. Amino acids 52 to 64 of SEQ ID NO:176 are a possible leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 65. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yi15_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yi15_1 should be approximately 2500 bp.

The nucleotide sequence disclosed herein for yi15_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yi15_1 demonstrated at least some similarity with sequences identified as AA290994 (zs45d07.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE 700429 5', mRNA sequence) and AF010235 (Homo sapiens mRNA from chromosome 5q31-33 region). Based upon sequence similarity, yi15_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts four potential transmembrane domains within the yi15_1 protein sequence, centered around amino acids 30, 60, 70, and 100 of SEQ ID NO:176, respectively.

Clone "yi17_1"

A polynucleotide of the present invention has been identified as clone "yi17_1". yi17_1 was isolated from a human brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yi17_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yi17_1 protein").

The nucleotide sequence of yi17_1 as presently determined is reported in SEQ ID NO:177, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yi17_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:178. Amino acids 6 to 18 of SEQ ID NO:178 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 19. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yi17_1 protein.

10 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yi17_1 should be approximately 1700 bp.

The nucleotide sequence disclosed herein for yi17_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yi17_1 demonstrated at least some similarity with sequences identified as AA418852 (zw01f10.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 15 768043 3', mRNA sequence). Based upon sequence similarity, yi17_1 proteins and each similar protein or peptide may share at least some activity.

Clone "yk38_1"

20 A polynucleotide of the present invention has been identified as clone "yk38_1". yk38_1 was isolated from a human adult thymus cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yk38_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yk38_1 protein").

25 The nucleotide sequence of yk38_1 as presently determined is reported in SEQ ID NO:179, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yk38_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:180. Amino acids 43 to 55 of SEQ ID NO:180 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 56. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yk38_1 protein.

30

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yk38_1 should be approximately 2050 bp.

The nucleotide sequence disclosed herein for yk38_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yk38_1 demonstrated at least some similarity with sequences identified as AA477698 (zu44c09.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 740848 5', mRNA sequence), AF052183 (Homo sapiens clone 24804 mRNA sequence), and T26733 (Human gene signature HUMGS08983; standard; cDNA to mRNA). Based upon sequence similarity, yk38_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts four potential transmembrane domains within the yk38_1 protein sequence, centered around amino acids 50, 135, 210 and 260 of SEQ ID NO:180, respectively. Hidden markov model and motifs analysis have revealed the presence of two WD-40 (beta transducin/G-beta) repeats at amino acids 118-153 and 157-196 of SEQ ID NO:180. The WD40 domain is thought to mediate protein-protein interactions.

Clone "yk51_1"

A polynucleotide of the present invention has been identified as clone "yk51_1". yk51_1 was isolated from a human adult thymus cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yk51_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yk51_1 protein").

The nucleotide sequence of yk51_1 as presently determined is reported in SEQ ID NO:181, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yk51_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:182. Amino acids 9 to 21 of SEQ ID NO:182 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 22. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a

The nucleotide sequence disclosed herein for yk51_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yk51_1 demonstrated at least some similarity with sequences identified as Z93014 (Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 167P19; HTGS phase 1). Based upon sequence similarity, yk51_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two additional potential transmembrane domains within the yk51_1 protein sequence, one centered around amino acid 65 and another around amino acid 81 of SEQ ID NO:182.

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Clone "yk74_1"

A polynucleotide of the present invention has been identified as clone "yk74_1". yk74_1 was isolated from a human adult thymus cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yk74_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yk74_1 protein").

The nucleotide sequence of yk74_1 as presently determined is reported in SEQ ID NO:183, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yk74_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:184.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yk74_1 should be approximately 1500 bp.

The nucleotide sequence disclosed herein for yk74_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yk74_1 demonstrated at least some similarity with sequences identified as AA910887 (ok87e02.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1520954 3', mRNA sequence). Based upon sequence similarity, yk74_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts three potential transmembrane domains within the yk74_1 protein sequence, centered around amino acids 15, 75, and 105 of SEQ ID NO:184, respectively. The nucleotide sequence of yk74_1 indicates that it may contain an Alu repetitive element.

Clone "yk89_1"

A polynucleotide of the present invention has been identified as clone "yk89_1". yk89_1 was isolated from a human adult thymus cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yk89_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yk89_1 protein").

The nucleotide sequence of yk89_1 as presently determined is reported in SEQ ID NO:185, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yk89_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:186.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yk89_1 should be approximately 2800 bp.

The nucleotide sequence disclosed herein for yk89_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yk89_1 demonstrated at least some similarity with sequences identified as AA524431 (ng44e05.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE 937664, mRNA sequence), AF045607 (Xenopus laevis origin recognition complex associated protein p81 mRNA, complete cds), U50950 (Human infant brain unknown product mRNA, complete cds), and V23269 (Human latheo protein encoding est cDNA; standard; cDNA). The predicted amino acid sequence disclosed herein for yk89_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted yk89_1 protein demonstrated at least some similarity to sequences identified as U50950 (unknown [Homo sapiens]), W53458 and W53460 (latheo protein [Drosophila]), W53459 (Human latheo protein sequence), and W53461 (Human latheo protein internal reading protein sequence). The *latheo* gene encodes a protein of ~70 kD which lacks sequence or domain homology to known proteins. *In situ* staining with a polyclonal antibody raised against the Latheo protein reveals protein expression in the larval central nervous system (CNS), and specific localization in presynaptic boutons at roughly half the neuromuscular junctions in 3rd-instar larvae, consistent with a role for Latheo protein in synaptic function. (Rohrbough, Pinto, and Tully, Center for Learning and Memory, Cold Spring Harbor Laboratory; and K.S. Broadie, Dept. of Biology, University of Utah, Salt Lake City UT 84112.) Based upon sequence similarity, yk89_1 proteins and each similar protein or peptide may share at least some

activity. The TopPredII computer program predicts a potential transmembrane domain within the yk89_1 protein sequence centered around amino acid 250 of SEQ ID NO:186.

Clone "yl18_1"

5 A polynucleotide of the present invention has been identified as clone "yl18_1". yl18_1 was isolated from a human adult spleen cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yl18_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yl18_1 protein").

10 The nucleotide sequence of yl18_1 as presently determined is reported in SEQ ID NO:187, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yl18_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:188. Amino acids 13 to 25 of SEQ ID NO:188 are a predicted leader/signal sequence, with the predicted mature
15 amino acid sequence beginning at amino acid 26. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yl18_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone
20 yl18_1 should be approximately 3116 bp.

The nucleotide sequence disclosed herein for yl18_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yl18_1 demonstrated at least some similarity with sequences identified as AA156907 (zl20b04.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA
25 clone 502447 5', mRNA sequence). Based upon sequence similarity, yl18_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts three additional potential transmembrane domains within the yl18_1 protein sequence, centered around amino acids 50, 105, and 115 of SEQ ID NO:188.

yl18_1 protein was expressed in a COS cell expression system, and an expressed
30 protein band of approximately 27 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "yb325_1"

A polynucleotide of the present invention has been identified as clone "yb325_1". yb325_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yb325_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yb325_1 protein").

The nucleotide sequence of yb325_1 as presently determined is reported in SEQ ID NO:189. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yb325_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:190. Amino acids 3 to 15 of SEQ ID NO:190 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 16. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yb325_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yb325_1 should be approximately 839 bp.

The nucleotide sequence disclosed herein for yb325_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yb325_1 demonstrated at least some similarity with sequences identified as AA523268 (ni39g02.s1 NCI_CGAP_Lu1 Homo sapiens cDNA clone IMAGE: 979250, mRNA sequence). Based upon sequence similarity, yb235_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional potential transmembrane domain within the yb235_1 protein sequence, centered around amino acid 90 of SEQ ID NO:188.

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Clone "yd261_1"

A polynucleotide of the present invention has been identified as clone "yd261_1". yd261_1 was isolated from a human adult brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yd261_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yd261_1 protein").

The nucleotide sequence of yd261_1 as presently determined is reported in SEQ ID NO:191, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yd261_1 protein

corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:192. Amino acids 25 to 37 of SEQ ID NO:192 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 38. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yd261_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yd261_1 should be approximately 491 bp.

The nucleotide sequence disclosed herein for yd261_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yd261_1 demonstrated at least some similarity with sequences identified as Q61280 (Human brain Expressed Sequence Tag EST01297; standard; DNA) and T15557 (IB1543 Infant brain, Bento Soares Homo sapiens cDNA 3' end similar to EST01297 H. sapiens cDNA clone HHCPN24, mRNA sequence). Based upon sequence similarity, yd261_1 proteins and each similar protein or peptide may share at least some activity.

Clone "yh33_1"

A polynucleotide of the present invention has been identified as clone "yh33_1". yh33_1 was isolated from a human brain (fetal and adult) cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yh33_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yh33_1 protein").

The nucleotide sequence of yh33_1 as presently determined is reported in SEQ ID NO:193, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yh33_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:194. Amino acids 80 to 92 of SEQ ID NO:194 are a possible leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 93. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yh33_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yh33_1 should be approximately 2750 bp.

The nucleotide sequence disclosed herein for yh33_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No significant hits were found in the database. The TopPredII computer program predicts three additional potential transmembrane domains within the yh33_1 protein sequence, centered around amino acids 124, 160, and 190 of SEQ ID NO:194, respectively. The nucleotide sequence of yh33_1 indicates that it may contain an Alu repetitive element.

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Clone "yi16_1"

A polynucleotide of the present invention has been identified as clone "yi16_1". yi16_1 was isolated from a human adult brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yi16_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yi16_1 protein").

The nucleotide sequence of yi16_1 as presently determined is reported in SEQ ID NO:195, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yi16_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:196. Amino acids 63 to 75 of SEQ ID NO:196 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 76. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yi16_1 protein.

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The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yi16_1 should be approximately 3000 bp.

The nucleotide sequence disclosed herein for yi16_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yi16_1 demonstrated at least some similarity with sequences identified as AI076775 (oz31f03.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE 1676957 3', mRNA sequence), T19914 (Human gene signature HUMGS01041; standard; cDNA to mRNA), and U79267 (Human clone 23840 mRNA, partial cds). The predicted amino acid sequence disclosed herein for yi16_1 was searched

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against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted yi16_1 protein demonstrated at least some similarity to the sequence identified as U79267 (unknown [Homo sapiens]). Based upon sequence similarity, yi16_1 proteins and each similar protein or peptide may share at least some activity.

Clone "yk46_1"

A polynucleotide of the present invention has been identified as clone "yk46_1". yk46_1 was isolated from a human adult thymus cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yk46_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yk46_1 protein").

The nucleotide sequence of yk46_1 as presently determined is reported in SEQ ID NO:197, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yk46_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:198. Amino acids 28 to 40 of SEQ ID NO:198 are a possible leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 41. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yk46_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yk46_1 should be approximately 1900 bp.

The nucleotide sequence disclosed herein for yk46_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yk46_1 demonstrated at least some similarity with sequences identified as AA203346 (zx56h01.r1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 446545 5', mRNA sequence). Based upon sequence similarity, yk46_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two additional potential transmembrane domains within the yk46_1 protein sequence, one centered around amino acid 20 and another around amino acid 57 of SEQ ID NO:198.

Clone "yk84_1"

A polynucleotide of the present invention has been identified as clone "yk84_1". yk84_1 was isolated from a human adult thymus cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yk84_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yk84_1 protein").

The nucleotide sequence of yk84_1 as presently determined is reported in SEQ ID NO:199, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yk84_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:200. Amino acids 36 to 48 of SEQ ID NO:200 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 49. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yk84_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yk84_1 should be approximately 2400 bp.

The nucleotide sequence disclosed herein for yk84_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yk84_1 demonstrated at least some similarity with sequences identified as AC004052 (Homo sapiens chromosome 4 clone B209B10 map 4q25, complete sequence) and AQ059417 (CIT-HSP-2348J2.TF CIT-HSP Homo sapiens genomic clone 2348J2, genomic survey sequence). Based upon sequence similarity, yk84_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the yk84_1 protein sequence, centered around amino acid 49 of SEQ ID NO:200.

Clone "yk143_1"

A polynucleotide of the present invention has been identified as clone "yk143_1". yk143_1 was isolated from a human adult thymus cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yk143_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yk143_1 protein").

The nucleotide sequence of yk143_1 as presently determined is reported in SEQ ID NO:201, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yk143_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:202.

- 5 Amino acids 31 to 43 of SEQ ID NO:202 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 44. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yk143_1 protein.

- 10 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yk143_1 should be approximately 1458 bp.

The nucleotide sequence disclosed herein for yk143_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yk143_1 demonstrated at least some similarity with sequences
15 identified as AA526186 (ni94h03.s1 NCI_CGAP_Pr21 Homo sapiens cDNA clone IMAGE:984533, mRNA sequence), AB006085 (Danio rerio mRNA for MINDIN2, complete cds), and T78360 (Human neuronal attachment factor-1 DNA; standard; DNA). The predicted amino acid sequence disclosed herein for yk143_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol.

- 20 The predicted yk143_1 protein demonstrated at least some similarity to sequences identified as AB006085 (MINDIN2 [Danio rerio]) and W23663 (Human neuronal attachment factor-1). Human neuronal attachment factor-1 is thought to promote cell-cell interaction and cell adhesion. The predicted yk143_1 protein also demonstrated at least some similarity to the extracellular matrix proteins called F- and M-spodins. Based upon
25 sequence similarity, yk143_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two additional potential transmembrane domains within the yk143_1 protein sequence, one centered around amino acid 204 and another around amino acid 280 of SEQ ID NO:202.

30 Clone "yk156_1"

A polynucleotide of the present invention has been identified as clone "yk156_1". yk156_1 was isolated from a human adult thymus cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the

amino acid sequence of the encoded protein. yk156_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yk156_1 protein").

The nucleotide sequence of yk156_1 as presently determined is reported in SEQ ID NO:203, and includes a poly(A) tail. What applicants presently believe to be the proper
5 reading frame and the predicted amino acid sequence of the yk156_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:204. Amino acids 25 to 37 of SEQ ID NO:204 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 38. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a
10 transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yk156_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yk156_1 should be approximately 1100 bp.

The nucleotide sequence disclosed herein for yk156_1 was searched against the
15 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yk156_1 demonstrated at least some similarity with sequences identified as AC002550 (Human Chromosome 16 BAC clone CIT987SK-A-101F10, complete sequence) and N67878 (yz52b04.s1 Homo sapiens cDNA clone 286639 3' similar to gb M29610 GLYCOPHORIN E PRECURSOR (HUMAN)). Based upon sequence
20 similarity, yk156_1 proteins and each similar protein or peptide may share at least some activity.

Clone "yk204_1"

A polynucleotide of the present invention has been identified as clone "yk204_1".
25 yk204_1 was isolated from a human adult thymus cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yk204_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yk204_1 protein").

The nucleotide sequence of yk204_1 as presently determined is reported in SEQ
30 ID NO:205, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yk204_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:206. Amino acids 46 to 58 of SEQ ID NO:206 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 59. Due to the

hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yk204_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone
5 yk204_1 should be approximately 1395 bp.

The nucleotide sequence disclosed herein for yk204_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No significant hits were found in the database. The TopPredII
10 computer program predicts two potential transmembrane domains within the yk204_1 protein sequence, one centered around amino acid 59 and another around amino acid 82 of SEQ ID NO:206. The nucleotide sequence of yk204_1 indicates that it may contain an Alu repetitive element.

Clone "yk224_1"

15 A polynucleotide of the present invention has been identified as clone "yk224_1". yk224_1 was isolated from a human adult thymus cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yk224_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yk224_1 protein").

20 The nucleotide sequence of yk224_1 as presently determined is reported in SEQ ID NO:207, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yk224_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:208. Amino acids 13 to 25 of SEQ ID NO:208 are a possible leader/signal sequence, with the
25 predicted mature amino acid sequence beginning at amino acid 26. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yk224_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone
30 yk224_1 should be approximately 1600 bp.

The nucleotide sequence disclosed herein for yk224_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yk224_1 demonstrated at least some similarity with sequences identified as AA789332 (aj28h05.s1 Soares testis NHT Homo sapiens cDNA clone 1391673

3' similar to WP:B0410.2 CE06708; mRNA sequence) and AF044208 (*Drosophila melanogaster* Strabismus (stbm) mRNA, complete cds). The predicted amino acid sequence disclosed herein for yk224_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted yk224_1 protein demonstrated at least some similarity to the sequence identified as AF044208 (Strabismus [*Drosophila melanogaster*]). Strabismus is described as a protein "that regulates tissue polarity and cell fate decisions in *Drosophila*" (Wolff, T. and Rubin, G.M., 1998, *Development* 125(6): 1149-1159, which is incorporated by reference herein). Based upon sequence similarity, yk224_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts four potential transmembrane domains within the yk224_1 protein sequence, centered around amino acids 26, 64, 98, and 134 of SEQ ID NO:208, respectively. The nucleotide sequence of yk224_1 indicates that it may contain an Alu repetitive element.

15 Clone "yk261_1"

A polynucleotide of the present invention has been identified as clone "yk261_1". yk261_1 was isolated from a human adult thymus cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yk261_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yk261_1 protein").

The nucleotide sequence of yk261_1 as presently determined is reported in SEQ ID NO:209, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yk261_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:210. Amino acids 13 to 25 of SEQ ID NO:210 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 26. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yk261_1 protein.

30 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yk261_1 should be approximately 2259 bp.

The nucleotide sequence disclosed herein for yk261_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yk261_1 demonstrated at least some similarity with sequences

identified as AI024733 (ov76e12.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1643278 3', mRNA sequence). The predicted amino acid sequence disclosed herein for yk261_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted yk261_1 protein
5 demonstrated at least some similarity to sequences identified as AF040650 (contains similarity to sodium-potassium-chloride cotransport proteins [Caenorhabditis elegans]), AF051561 (similarity to sodium-potassium-chloride cotransport proteins [rat]), U13174 (putative basolateral Na-K-2Cl cotransporter [Mus musculus]), U55054 (K-Cl cotransporter [Homo sapiens]), and Z36104 (similarity to sodium-potassium-chloride
10 cotransport proteins [yeast]). Based upon sequence similarity, yk261_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two additional potential transmembrane domains within the yk261_1 protein sequence, one centered around amino acid 270 and another around amino acid 295 of SEQ ID NO:210.

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Clone "ys3_1"

A polynucleotide of the present invention has been identified as clone "ys3_1". ys3_1 was isolated from a human adult thymus cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the
20 amino acid sequence of the encoded protein. ys3_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ys3_1 protein").

The nucleotide sequence of ys3_1 as presently determined is reported in SEQ ID NO:211, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the ys3_1 protein corresponding
25 to the foregoing nucleotide sequence is reported in SEQ ID NO:212. Amino acids 112 to 124 of SEQ ID NO:212 are a possible leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 125. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the ys3_1
30 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ys3_1 should be approximately 1000 bp.

The nucleotide sequence disclosed herein for ys3_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and

FASTA search protocols. ys3_1 demonstrated at least some similarity with sequences identified as H93009 (yv07g03.s1 Homo sapiens cDNA clone 242068 3'). The predicted amino acid sequence disclosed herein for ys3_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The
5 predicted ys3_1 protein demonstrated at least some similarity to sequences identified as L35848 (IgE receptor beta subunit [Homo sapiens]) and R42337 (Human FcεRI beta). Based upon sequence similarity, ys3_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts five potential transmembrane domains within the ys3_1 protein sequence, centered around amino acids
10 60, 90, 125, 190, and 225 of SEQ ID NO:212, respectively.

ys3_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 26 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

15 Clone "ys10_1"

A polynucleotide of the present invention has been identified as clone "ys10_1". ys10_1 was isolated from a human adult thymus cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. ys10_1 is a full-length clone, including the
20 entire coding sequence of a secreted protein (also referred to herein as "ys10_1 protein").

The nucleotide sequence of ys10_1 as presently determined is reported in SEQ ID NO:213, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the ys10_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:214. Amino acids 30 to
25 42 of SEQ ID NO:214 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 43. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the ys10_1 protein.

30 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ys10_1 should be approximately 1079 bp.

The nucleotide sequence disclosed herein for ys10_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ys10_1 demonstrated at least some similarity with sequences

identified as AA436002 (zu03b10.s1 Soares testis NHT Homo sapiens cDNA clone 730747 3', mRNA sequence) and T26591 (Human gene signature HUMGS08837; standard; cDNA to mRNA). Based upon sequence similarity, ys10_1 proteins and each similar protein or peptide may share at least some activity.

5

Deposit of Clones

Clones ya15_1, ya24_1, yb42_1, yc9_1, yc19_1, and yc20_1 were deposited on February 11, 1998 with the American Type Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the
10 Budapest Treaty and were given the accession number ATCC 98650, from which each clone comprising a particular polynucleotide is obtainable.

Clones ya9_1, ya11_1, ya28_1, yb81_1, and yc14_1 were deposited on April 7, 1998 with the American Type Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were
15 given the accession number ATCC 98724, from which each clone comprising a particular polynucleotide is obtainable.

Clones yc24_1, yc25_1, and ye2_1 were deposited on May 14, 1998 with the American Type Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the
20 accession number ATCC 98755, from which each clone comprising a particular polynucleotide is obtainable.

Clones ya65_1, yb60_1, yb139_1, yc29_1, yc40_1, yd10_1, and yf5_1 were deposited on August 11, 1998 with the American Type Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under
25 the Budapest Treaty and were given the accession number ATCC 98834, from which each clone comprising a particular polynucleotide is obtainable.

Clones ya67_1, ya70_1, yb51_1, yb101_1, yb124_1, yb125_1, yb179_1, yc48_1, ye21_1, and ye22_1 were deposited on September 3, 1998 with the American Type Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an
30 original deposit under the Budapest Treaty and were given the accession number ATCC 98864, from which each clone comprising a particular polynucleotide is obtainable.

Clones ye39_1, yf9_1, yh4_1, yi4_1, yj3_1, yj7_1, yj10_1, yj28_1, yj29_1, and yj32_1 were deposited on September 2, 1998 with the American Type Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under

the Budapest Treaty and were given the accession number ATCC 98861, from which each clone comprising a particular polynucleotide is obtainable.

Clones yb186_1, yb226_1, yd50_1, yd51_1, yd73_1, ye43_1, yh71_1, yh100_1, yi3_1, yj23_1, and yl9_1 were deposited on September 10, 1998 with the American Type Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number ATCC 98872, from which each clone comprising a particular polynucleotide is obtainable.

Clones ya66_1, yb187_1, yb219_1, yb228_1, yc27_1, yc49_1, yd40_1, yd64_1, ye47_1, yh50_1, yh53_1, and yh98_1 were deposited on September 23, 1998 with the American Type Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number ATCC 98887, from which each clone comprising a particular polynucleotide is obtainable.

Clones ya69_1, yd107_1, yd145_1, yh24_1, yi11_1, yi18_1, yk14_1, yk39_1, yk91_1, yk199_1, yl4_1, and yl14_1 were deposited on October 6, 1998 with the American Type Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number ATCC 98915, from which each clone comprising a particular polynucleotide is obtainable.

Clones ya80_1, yd61_1, yd88_1, yd109_1, yd141_1, yd153_1, yd165_1, yd178_1, and yd191_1 were deposited on October 15, 1998 with the American Type Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number ATCC 98925, from which each clone comprising a particular polynucleotide is obtainable.

Clones ye7_1, yf33_1, yi15_1, yi17_1, yk38_1, yk51_1, yk74_1, yk89_1, and yl18_1 were deposited on October 15, 1998 with the American Type Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number ATCC 98924, from which each clone comprising a particular polynucleotide is obtainable.

Clones yb235_1, yd261_1, yh33_1, yi16_1, yk46_1, yk84_1, yk143_1, yk156_1, yk204_1, yk224_1, yk261_1, ys3_1, and ys10_1 were deposited on October 27, 1998 with the American Type Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number ATCC 98958, from which each clone comprising a particular polynucleotide is obtainable.

All restrictions on the availability to the public of the deposited material will be irrevocably removed upon the granting of the patent, except for the requirements specified in 37 C.F.R. § 1.808(b), and the term of the deposit will comply with 37 C.F.R. § 1.806.

5 Each clone has been transfected into separate bacterial cells (*E. coli*) in these composite deposits. Each clone can be removed from the vector in which it was deposited by performing an EcoRI/NotI digestion (5' site, EcoRI; 3' site, NotI) to produce the appropriate fragment for such clone. Each clone was deposited in either the pED6 or pNOTs vector depicted in Figures 1A and 1B, respectively. The pED6dpc2 vector
10 ("pED6") was derived from pED6dpc1 by insertion of a new polylinker to facilitate cDNA cloning (Kaufman *et al.*, 1991, *Nucleic Acids Res.* 19: 4485-4490); the pNOTs vector was derived from pMT2 (Kaufman *et al.*, 1989, *Mol. Cell. Biol.* 9: 946-958) by deletion of the DHFR sequences, insertion of a new polylinker, and insertion of the M13 origin of replication in the ClaI site. In some instances, the deposited clone can become "flipped"
15 (i.e., in the reverse orientation) in the deposited isolate. In such instances, the cDNA insert can still be isolated by digestion with EcoRI and NotI. However, NotI will then produce the 5' site and EcoRI will produce the 3' site for placement of the cDNA in proper orientation for expression in a suitable vector. The cDNA may also be expressed from the vectors in which they were deposited.

20 Bacterial cells containing a particular clone can be obtained from the composite deposit as follows:

An oligonucleotide probe or probes should be designed to the sequence that is known for that particular clone. This sequence can be derived from the sequences provided herein, or from a combination of those sequences. The sequence of an
25 oligonucleotide probe that was used to isolate or to sequence each full-length clone is identified below, and should be most reliable in isolating the clone of interest.

<u>Clone</u>	<u>Probe Sequence</u>
ya15_1	SEQ ID NO:215
30 ya24_1	SEQ ID NO:216
yb42_1	SEQ ID NO:217
yc9_1	SEQ ID NO:218
yc19_1	SEQ ID NO:219
yc20_1	SEQ ID NO:220

	ya9_1	SEQ ID NO:221
	ya28_1	SEQ ID NO:222
	yc14_1	SEQ ID NO:223
	yc24_1	SEQ ID NO:224
5	yc25_1	SEQ ID NO:225
	ye2_1	SEQ ID NO:226
	yb60_1	SEQ ID NO:227
	yc29_1	SEQ ID NO:228
	yf5_1	SEQ ID NO:229
10	ya70_1	SEQ ID NO:230
	yb51_1	SEQ ID NO:231
	yb101_1	SEQ ID NO:232
	yb124_1	SEQ ID NO:233
	yb125_1	SEQ ID NO:234
15	yb179_1	SEQ ID NO:235
	ye21_1	SEQ ID NO:236
	ye22_1	SEQ ID NO:237
	yf9_1	SEQ ID NO:238
	yh71_1	SEQ ID NO:239
20	yh100_1	SEQ ID NO:240
	yj23_1	SEQ ID NO:241
	yb187_1	SEQ ID NO:242
	yb219_1	SEQ ID NO:243
	yd40_1	SEQ ID NO:244
25	ye47_1	SEQ ID NO:245
	yh50_1	SEQ ID NO:246
	yh53_1	SEQ ID NO:247
	ya69_1	SEQ ID NO:248
	yi11_1	SEQ ID NO:249
30	yl4_1	SEQ ID NO:250
	ye7_1	SEQ ID NO:251
	yf33_1	SEQ ID NO:252
	yi15_1	SEQ ID NO:253
	yi17_1	SEQ ID NO:254

	yk38_1	SEQ ID NO:255
	yk89_1	SEQ ID NO:256
	yl18_1	SEQ ID NO:257
	yh33_1	SEQ ID NO:258
5	yi16_1	SEQ ID NO:259
	yk46_1	SEQ ID NO:260
	yk84_1	SEQ ID NO:261
	yk204_1	SEQ ID NO:262
	yk224_1	SEQ ID NO:263
10	yk261_1	SEQ ID NO:264

In the sequences listed above which include an N at position 2, that position is occupied in preferred probes/primers by a biotinylated phosphoramidite residue rather than a nucleotide (such as, for example, that produced by use of biotin phosphoramidite (1-dimethoxytrityloxy-2-(N-biotinyl-4-aminobutyl)-propyl-3-O-(2-cyanoethyl)-(N,N-diisopropyl)-phosphoramidite) (Glen Research, cat. no. 10-1953)).

The design of the oligonucleotide probe should preferably follow these parameters:

- (a) It should be designed to an area of the sequence which has the fewest ambiguous bases ("N's"), if any;
- (b) It should be designed to have a T_m of approx. 80 °C (assuming 2° for each A or T and 4 degrees for each G or C).

The oligonucleotide should preferably be labeled with γ -³²P ATP (specific activity 6000 Ci/mmol) and T4 polynucleotide kinase using commonly employed techniques for labeling oligonucleotides. Other labeling techniques can also be used. Unincorporated label should preferably be removed by gel filtration chromatography or other established methods. The amount of radioactivity incorporated into the probe should be quantitated by measurement in a scintillation counter. Preferably, specific activity of the resulting probe should be approximately 4e+6 dpm/pmol.

The bacterial culture containing the pool of full-length clones should preferably be thawed and 100 μ l of the stock used to inoculate a sterile culture flask containing 25 ml of sterile L-broth containing ampicillin at 100 μ g/ml. The culture should preferably be grown to saturation at 37°C, and the saturated culture should preferably be diluted in fresh L-broth. Aliquots of these dilutions should preferably be plated to determine the

dilution and volume which will yield approximately 5000 distinct and well-separated colonies on solid bacteriological media containing L-broth containing ampicillin at 100 µg/ml and agar at 1.5% in a 150 mm petri dish when grown overnight at 37°C. Other known methods of obtaining distinct, well-separated colonies can also be employed.

- 5 Standard colony hybridization procedures should then be used to transfer the colonies to nitrocellulose filters and lyse, denature and bake them.

- The filter is then preferably incubated at 65°C for 1 hour with gentle agitation in 6X SSC (20X stock is 175.3 g NaCl/liter, 88.2 g Na citrate/liter, adjusted to pH 7.0 with NaOH) containing 0.5% SDS, 100 µg/ml of yeast RNA, and 10 mM EDTA (approximately
10 10 mL per 150 mm filter). Preferably, the probe is then added to the hybridization mix at a concentration greater than or equal to 1e+6 dpm/mL. The filter is then preferably incubated at 65°C with gentle agitation overnight. The filter is then preferably washed in 500 mL of 2X SSC/0.5% SDS at room temperature without agitation, preferably followed by 500 mL of 2X SSC/0.1% SDS at room temperature with gentle shaking for 15 minutes.
15 A third wash with 0.1X SSC/0.5% SDS at 65°C for 30 minutes to 1 hour is optional. The filter is then preferably dried and subjected to autoradiography for sufficient time to visualize the positives on the X-ray film. Other known hybridization methods can also be employed.

- The positive colonies are picked, grown in culture, and plasmid DNA isolated
20 using standard procedures. The clones can then be verified by restriction analysis, hybridization analysis, or DNA sequencing.

- Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example,
25 as described in H.U. Saragovi, *et al.*, Bio/Technology 10, 773-778 (1992) and in R.S. McDowell, *et al.*, J. Amer. Chem. Soc. 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites. For example, fragments of the protein may be fused through "linker" sequences to
30 the Fc portion of an immunoglobulin. For a bivalent form of the protein, such a fusion could be to the Fc portion of an IgG molecule. Other immunoglobulin isotypes may also be used to generate such fusions. For example, a protein - IgM fusion would generate a decavalent form of the protein of the invention.

The present invention also provides both full-length and mature forms of the disclosed proteins. The full-length form of the such proteins is identified in the sequence listing by translation of the nucleotide sequence of each disclosed clone. The mature form(s) of such protein may be obtained by expression of the disclosed full-length
5 polynucleotide (preferably those deposited with ATCC) in a suitable mammalian cell or other host cell. The sequence(s) of the mature form(s) of the protein may also be determinable from the amino acid sequence of the full-length form.

The present invention also provides genes corresponding to the polynucleotide sequences disclosed herein. "Corresponding genes" are the regions of the genome that
10 are transcribed to produce the mRNAs from which cDNA polynucleotide sequences are derived and may include contiguous regions of the genome necessary for the regulated expression of such genes. Corresponding genes may therefore include but are not limited to coding sequences, 5' and 3' untranslated regions, alternatively spliced exons, introns, promoters, enhancers, and silencer or suppressor elements. The corresponding genes can
15 be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. An "isolated gene" is a gene that has been separated from the adjacent coding sequences, if any, present in the genome of
20 the organism from which the gene was isolated.

The chromosomal location corresponding to the polynucleotide sequences disclosed herein may also be determined, for example by hybridizing appropriately labeled polynucleotides of the present invention to chromosomes *in situ*. It may also be possible to determine the corresponding chromosomal location for a disclosed
25 polynucleotide by identifying significantly similar nucleotide sequences in public databases, such as expressed sequence tags (ESTs), that have already been mapped to particular chromosomal locations. For at least some of the polynucleotide sequences disclosed herein, public database sequences having at least some similarity to the polynucleotide of the present invention have been listed by database accession number.
30 Searches using the GenBank accession numbers of these public database sequences can then be performed at an Internet site provided by the National Center for Biotechnology Information having the address <http://www.ncbi.nlm.nih.gov/UniGene/>, in order to identify "UniGene clusters" of overlapping sequences. Many of the "UniGene clusters" so identified will already have been mapped to particular chromosomal sites.

Organisms that have enhanced, reduced, or modified expression of the gene(s) corresponding to the polynucleotide sequences disclosed herein are provided. The desired change in gene expression can be achieved through the use of antisense polynucleotides or ribozymes that bind and/or cleave the mRNA transcribed from the gene (Albert and Morris, 1994, *Trends Pharmacol. Sci.* 15(7): 250-254; Lavarosky *et al.*, 1997, *Biochem. Mol. Med.* 62(1): 11-22; and Hampel, 1998, *Prog. Nucleic Acid Res. Mol. Biol.* 58: 1-39; all of which are incorporated by reference herein). Transgenic animals that have multiple copies of the gene(s) corresponding to the polynucleotide sequences disclosed herein, preferably produced by transformation of cells with genetic constructs that are stably maintained within the transformed cells and their progeny, are provided. Transgenic animals that have modified genetic control regions that increase or reduce gene expression levels, or that change temporal or spatial patterns of gene expression, are also provided (see European Patent No. 0 649 464 B1, incorporated by reference herein). In addition, organisms are provided in which the gene(s) corresponding to the polynucleotide sequences disclosed herein have been partially or completely inactivated, through insertion of extraneous sequences into the corresponding gene(s) or through deletion of all or part of the corresponding gene(s). Partial or complete gene inactivation can be accomplished through insertion, preferably followed by imprecise excision, of transposable elements (Plasterk, 1992, *Bioessays* 14(9): 629-633; Zwaal *et al.*, 1993, *Proc. Natl. Acad. Sci. USA* 90(16): 7431-7435; Clark *et al.*, 1994, *Proc. Natl. Acad. Sci. USA* 91(2): 719-722; all of which are incorporated by reference herein), or through homologous recombination, preferably detected by positive/negative genetic selection strategies (Mansour *et al.*, 1988, *Nature* 336: 348-352; U.S. Patent Nos. 5,464,764; 5,487,992; 5,627,059; 5,631,153; 5,614,396; 5,616,491; and 5,679,523; all of which are incorporated by reference herein). These organisms with altered gene expression are preferably eukaryotes and more preferably are mammals. Such organisms are useful for the development of non-human models for the study of disorders involving the corresponding gene(s), and for the development of assay systems for the identification of molecules that interact with the protein product(s) of the corresponding gene(s).

Where the protein of the present invention is membrane-bound (e.g., is a receptor), the present invention also provides for soluble forms of such protein. In such forms, part or all of the intracellular and transmembrane domains of the protein are deleted such that the protein is fully secreted from the cell in which it is expressed. The intracellular and transmembrane domains of proteins of the invention can be identified in accordance with

known techniques for determination of such domains from sequence information. For example, the TopPredII computer program can be used to predict the location of transmembrane domains in an amino acid sequence, domains which are described by the location of the center of the transmembrane domain, with at least ten transmembrane amino acids on each side of the reported central residue(s).

Proteins and protein fragments of the present invention include proteins with amino acid sequence lengths that are at least 25% (more preferably at least 50%, and most preferably at least 75%) of the length of a disclosed protein and have at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or 95% identity) with that disclosed protein, where sequence identity is determined by comparing the amino acid sequences of the proteins when aligned so as to maximize overlap and identity while minimizing sequence gaps. Also included in the present invention are proteins and protein fragments that contain a segment preferably comprising 8 or more (more preferably 20 or more, most preferably 30 or more) contiguous amino acids that shares at least 75% sequence identity (more preferably, at least 85% identity; most preferably at least 95% identity) with any such segment of any of the disclosed proteins.

In particular, sequence identity may be determined using WU-BLAST (Washington University BLAST) version 2.0 software, which builds upon WU-BLAST version 1.4, which in turn is based on the public domain NCBI-BLAST version 1.4 (Altschul and Gish, 1996, Local alignment statistics, Doolittle *ed.*, *Methods in Enzymology* 266: 460-480; Altschul *et al.*, 1990, Basic local alignment search tool, *Journal of Molecular Biology* 215: 403-410; Gish and States, 1993, Identification of protein coding regions by database similarity search, *Nature Genetics* 3: 266-272; Karlin and Altschul, 1993, Applications and statistics for multiple high-scoring segments in molecular sequences, *Proc. Natl. Acad. Sci. USA* 90: 5873-5877; all of which are incorporated by reference herein). WU-BLAST version 2.0 executable programs for several UNIX platforms can be downloaded from <ftp://blast.wustl.edu/blast/executables>. The complete suite of search programs (BLASTP, BLASTN, BLASTX, TBLASTN, and TBLASTX) is provided at that site, in addition to several support programs. WU-BLAST 2.0 is copyrighted and may not be sold or redistributed in any form or manner without the express written consent of the author; but the posted executables may otherwise be freely used for commercial, nonprofit, or academic purposes. In all search programs in the suite

-- BLASTP, BLASTN, BLASTX, TBLASTN and TBLASTX -- the gapped alignment routines are integral to the database search itself, and thus yield much better sensitivity and selectivity while producing the more easily interpreted output. Gapping can optionally be turned off in all of these programs, if desired. The default penalty (Q) for a gap of length one is Q=9 for proteins and BLASTP, and Q=10 for BLASTN, but may be changed to any integer value including zero, one through eight, nine, ten, eleven, twelve through twenty, twenty-one through fifty, fifty-one through one hundred, etc. The default per-residue penalty for extending a gap (R) is R=2 for proteins and BLASTP, and R=10 for BLASTN, but may be changed to any integer value including zero, one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve through twenty, twenty-one through fifty, fifty-one through one hundred, etc. Any combination of values for Q and R can be used in order to align sequences so as to maximize overlap and identity while minimizing sequence gaps. The default amino acid comparison matrix is BLOSUM62, but other amino acid comparison matrices such as PAM can be utilized.

Species homologues of the disclosed polynucleotides and proteins are also provided by the present invention. As used herein, a "species homologue" is a protein or polynucleotide with a different species of origin from that of a given protein or polynucleotide, but with significant sequence similarity to the given protein or polynucleotide. Preferably, polynucleotide species homologues have at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% identity) with the given polynucleotide, and protein species homologues have at least 30% sequence identity (more preferably, at least 45% identity; most preferably at least 60% identity) with the given protein, where sequence identity is determined by comparing the nucleotide sequences of the polynucleotides or the amino acid sequences of the proteins when aligned so as to maximize overlap and identity while minimizing sequence gaps. Species homologues may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species. Preferably, species homologues are those isolated from mammalian species. Most preferably, species homologues are those isolated from certain mammalian species such as, for example, *Pan troglodytes*, *Gorilla gorilla*, *Pongo pygmaeus*, *Hylobates concolor*, *Macaca mulatta*, *Papio papio*, *Papio hamadryas*, *Cercopithecus aethiops*, *Cebus capucinus*, *Aotus trivirgatus*, *Sanguinus oedipus*, *Microcebus murinus*, *Mus musculus*, *Rattus norvegicus*,

Cricetulus griseus, *Felis catus*, *Mustela vison*, *Canis familiaris*, *Oryctolagus cuniculus*, *Bos taurus*, *Ovis aries*, *Sus scrofa*, and *Equus caballus*, for which genetic maps have been created allowing the identification of syntenic relationships between the genomic organization of genes in one species and the genomic organization of the related genes in another species

5 (O'Brien and Seuánez, 1988, *Ann. Rev. Genet.* 22: 323-351; O'Brien *et al.*, 1993, *Nature Genetics* 3:103-112; Johansson *et al.*, 1995, *Genomics* 25: 682-690; Lyons *et al.*, 1997, *Nature Genetics* 15: 47-56; O'Brien *et al.*, 1997, *Trends in Genetics* 13(10): 393-399; Carver and Stubbs, 1997, *Genome Research* 7:1123-1137; all of which are incorporated by reference herein).

The invention also encompasses allelic variants of the disclosed polynucleotides

10 or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotides which also encode proteins which are identical or have significantly similar sequences to those encoded by the disclosed polynucleotides. Preferably, allelic variants have at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% identity) with the given polynucleotide, where sequence identity is determined by

15 comparing the nucleotide sequences of the polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps. Allelic variants may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from individuals of the appropriate species.

The invention also includes polynucleotides with sequences complementary to

20 those of the polynucleotides disclosed herein.

The present invention also includes polynucleotides that hybridize under reduced stringency conditions, more preferably stringent conditions, and most preferably highly stringent conditions, to polynucleotides described herein. Examples of stringency conditions are shown in the table below: highly stringent conditions are those that are at

25 least as stringent as, for example, conditions A-F; stringent conditions are at least as stringent as, for example, conditions G-L; and reduced stringency conditions are at least as stringent as, for example, conditions M-R.

Stringency Condition	Polynucleotide Hybrid	Hybrid Length (bp) [‡]	Hybridization Temperature and Buffer [†]	Wash Temperature and Buffer [†]
5	A	≥ 50	65°C; 1xSSC -or- 42°C; 1xSSC, 50% formamide	65°C; 0.3xSSC
	B	<50	T _B *; 1xSSC	T _B *; 1xSSC
	C	≥ 50	67°C; 1xSSC -or- 45°C; 1xSSC, 50% formamide	67°C; 0.3xSSC
	D	<50	T _D *; 1xSSC	T _D *; 1xSSC
	E	≥ 50	70°C; 1xSSC -or- 50°C; 1xSSC, 50% formamide	70°C; 0.3xSSC
	F	<50	T _F *; 1xSSC	T _F *; 1xSSC
10	G	≥ 50	65°C; 4xSSC -or- 42°C; 4xSSC, 50% formamide	65°C; 1xSSC
	H	<50	T _H *; 4xSSC	T _H *; 4xSSC
	I	≥ 50	67°C; 4xSSC -or- 45°C; 4xSSC, 50% formamide	67°C; 1xSSC
	J	<50	T _J *; 4xSSC	T _J *; 4xSSC
	K	≥ 50	70°C; 4xSSC -or- 50°C; 4xSSC, 50% formamide	67°C; 1xSSC
	L	<50	T _L *; 2xSSC	T _L *; 2xSSC
15	M	≥ 50	50°C; 4xSSC -or- 40°C; 6xSSC, 50% formamide	50°C; 2xSSC
	N	<50	T _N *; 6xSSC	T _N *; 6xSSC
	O	≥ 50	55°C; 4xSSC -or- 42°C; 6xSSC, 50% formamide	55°C; 2xSSC
	P	<50	T _P *; 6xSSC	T _P *; 6xSSC
	Q	≥ 50	60°C; 4xSSC -or- 45°C; 6xSSC, 50% formamide	60°C; 2xSSC
	R	<50	T _R *; 4xSSC	T _R *; 4xSSC

[‡] The hybrid length is that anticipated for the hybridized region(s) of the hybridizing polynucleotides. When hybridizing a polynucleotide to a target polynucleotide of unknown sequence, the hybrid length is assumed to be that of the hybridizing polynucleotide. When polynucleotides of known sequence are hybridized, the hybrid length can be determined by aligning the sequences of the polynucleotides and identifying the region or regions of optimal sequence complementarity.

[†] SSPE (1xSSPE is 0.15M NaCl, 10mM NaH₂PO₄, and 1.25mM EDTA, pH 7.4) can be substituted for SSC (1xSSC is 0.15M NaCl and 15mM sodium citrate) in the hybridization and wash buffers; washes are performed for 15 minutes after hybridization is complete.

*T_B - T_R: The hybridization temperature for hybrids anticipated to be less than 50 base pairs in length should be 5-10°C less than the melting temperature (T_m) of the hybrid, where T_m is determined according to the following equations. For hybrids less than 18 base pairs in length, T_m(°C) = 2(# of A + T bases) + 4(# of G + C bases). For hybrids between 18 and 49 base pairs in length, T_m(°C) = 81.5 + 16.6(log₁₀[Na⁺]) + 0.41(%G+C) - (600/N), where N is the number of bases in the hybrid, and [Na⁺] is the concentration of sodium ions in the hybridization buffer ([Na⁺] for 1xSSC = 0.165 M).

Additional examples of stringency conditions for polynucleotide hybridization are provided in Sambrook, J., E.F. Fritsch, and T. Maniatis, 1989, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, chapters 9 and 11, and *Current Protocols in Molecular Biology*, 1995, F.M. Ausubel et al., eds.,
5 John Wiley & Sons, Inc., sections 2.10 and 6.3-6.4, incorporated herein by reference.

Preferably, each such hybridizing polynucleotide has a length that is at least 25% (more preferably at least 50%, and most preferably at least 75%) of the length of the polynucleotide of the present invention to which it hybridizes, and has at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or
10 95% identity) with the polynucleotide of the present invention to which it hybridizes, where sequence identity is determined by comparing the sequences of the hybridizing polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps.

The isolated polynucleotide encoding the protein of the invention may be operably
15 linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman *et al.*, *Nucleic Acids Res.* 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, *Methods in Enzymology* 185, 537-566 (1990). As defined
20 herein "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

A number of types of cells may act as suitable host cells for expression of the
25 protein. Mammalian host cells include, for example, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells.

30 Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any bacterial

strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, e.g., Invitrogen, San Diego, California, U.S.A. (the MaxBac® kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (i.e., from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl® or Cibacrom blue 3GA Sepharose®; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX). Kits for expression and purification of such fusion proteins are commercially available from New England BioLabs (Beverly, MA), Pharmacia (Piscataway, NJ) and Invitrogen Corporation (Carlsbad, CA), respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("Flag") is commercially available from the Eastman Kodak Company (New Haven, CT).

Finally, one or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The protein may also be produced by known conventional chemical synthesis. Methods for constructing the proteins of the present invention by synthetic means are known to those skilled in the art. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications in the peptide or DNA sequences can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Patent No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and may thus be useful for screening or other immunological methodologies may also be easily made by those skilled in the art

given the disclosures herein. Such modifications are believed to be encompassed by the present invention.

USES AND BIOLOGICAL ACTIVITY

5 The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified below. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or by administration or use of polynucleotides encoding such proteins (such as, for example, in gene therapies
10 or vectors suitable for introduction of DNA).

Research Uses and Utilities

 The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express
15 recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on Southern gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare
20 with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for
25 examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, those
30 described in Gyuris *et al.*, 1993, *Cell* 75: 791-803 and in Rossi *et al.*, 1997, *Proc. Natl. Acad. Sci. USA* 94: 8405-8410, all of which are incorporated by reference herein) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The proteins provided by the present invention can similarly be used in assay to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine
5 levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Where the protein binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the
10 protein can be used to identify the other protein with which binding occurs or to identify inhibitors of the binding interaction. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent
15 grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E.F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to
20 Molecular Cloning Techniques", Academic Press, Berger, S.L. and A.R. Kimmel eds., 1987.

Nutritional Uses

Polynucleotides and proteins of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein
25 or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the protein or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the protein or polynucleotide of the invention
30 can be added to the medium in or on which the microorganism is cultured.

Cytokine and Cell Proliferation/Differentiation Activity

A protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may

induce production of other cytokines in certain cell populations. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for T-cell or thymocyte proliferation include without limitation those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., *J. Immunol.* 137:3494-3500, 1986; Bertagnolli et al., *J. Immunol.* 145:1706-1712, 1990; Bertagnolli et al., *Cellular Immunology* 133:327-341, 1991; Bertagnolli, et al., *J. Immunol.* 149:3778-3783, 1992; Bowman et al., *J. Immunol.* 152: 1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A.M. and Shevach, E.M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human Interferon γ , Schreiber, R.D. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L.S. and Lipsky, P.E. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., *J. Exp. Med.* 173:1205-1211, 1991; Moreau et al., *Nature* 336:690-692, 1988; Greenberger et al., *Proc. Natl. Acad. Sci. U.S.A.* 80:2931-2938, 1983; Measurement of mouse and human interleukin 6 - Nordan, R. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., *Proc. Natl. Acad. Sci. U.S.A.* 83:1857-1861, 1986; Measurement of human Interleukin 11 - Bennett, F., Giannotti, J., Clark, S.C. and Turner, K. J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991;

Measurement of mouse and human Interleukin 9 - Ciarletta, A., Giannotti, J., Clark, S.C. and Turner, K.J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

Immune Stimulating or Suppressing Activity

A protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, *Leishmania* spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease.

Such a protein of the present invention may also be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present
5 invention.

Using the proteins of the invention it may also be possible to regulate immune responses in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by
10 suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and
15 persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as , for example, B7)), *e.g.*, preventing
20 high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys
25 the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (*e.g.*, B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the
30 molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this matter prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term

tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

5 The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins *in vivo* as
10 described in Lenschow *et al.*, Science 257:789-792 (1992) and Turka *et al.*, Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function *in vivo* on the development of that disease.

15 Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms.
20 Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from
25 the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythematosus in MRL/*lpr/lpr* mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and
30 murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune

response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells *in vitro* with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the *in vitro* activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells *in vivo*.

In another application, up regulation or enhancement of antigen function (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (*e.g.*, sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected *ex vivo* with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection *in vivo*.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (*e.g.*, a cytoplasmic-domain truncated portion) of an MHC class I α chain protein and β_2

microglobulin protein or an MHC class II α chain protein and an MHC class II β chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated
 5 immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated
 10 immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without
 15 limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al.,
 20 J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Bowman et al., J. Virology 61:1992-1998; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnoli et al.,
 25 Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: *In vitro*
 30 antibody production, Mond, J.J. and Brunswick, M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek,

D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

- 5 Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995;
- 10 Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

- Assays for lymphocyte survival/apoptosis (which will identify, among others,
- 15 proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993;
- 20 Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

25

Hematopoiesis Regulating Activity

- A protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell
- 30 lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid

cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M.G. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, NY. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I.K. and Briddell, R.A. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, NY. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R.E. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, NY. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and

Allen, T. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, NY. 1994; Long term culture initiating cell assay, Sutherland, H.J. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, NY. 1994.

5

Tissue Growth Activity

A protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns,
10 incisions and ulcers.

A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as
15 well as open fracture reduction and also in the improved fixation of artificial joints. *De novo* bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal
20 disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue
25 destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in
30 circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and

in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation

of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, HI and Rovee, DT, eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

Activin/Inhibin Activity

A protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention, alone or in heterodimers with a member of the inhibin α family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin- β group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, United States Patent 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

Chemotactic/Chemokinetic Activity

A protein of the present invention may have chemotactic or chemokinetic activity (e.g., act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al.

APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25: 1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153: 1762-1768, 1994.

Hemostatic and Thrombolytic Activity

5 A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting
10 formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

 The activity of a protein of the invention may, among other means, be measured by the following methods:

15 Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

20 Receptor/Ligand Activity

 A protein of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands,
25 receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant
30 receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

 The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static
5 conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

10 Anti-Inflammatory Activity

Proteins of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the
15 inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic
20 inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

25

Cadherin/Tumor Invasion Suppressor Activity

Cadherins are calcium-dependent adhesion molecules that appear to play major roles during development, particularly in defining specific cell types. Loss or alteration of normal cadherin expression can lead to changes in cell adhesion properties linked to
30 tumor growth and metastasis. Cadherin malfunction is also implicated in other human diseases, such as pemphigus vulgaris and pemphigus foliaceus (auto-immune blistering skin diseases), Crohn's disease, and some developmental abnormalities.

The cadherin superfamily includes well over forty members, each with a distinct pattern of expression. All members of the superfamily have in common conserved

extracellular repeats (cadherin domains), but structural differences are found in other parts of the molecule. The cadherin domains bind calcium to form their tertiary structure and thus calcium is required to mediate their adhesion. Only a few amino acids in the first cadherin domain provide the basis for homophilic adhesion; modification of this
5 recognition site can change the specificity of a cadherin so that instead of recognizing only itself, the mutant molecule can now also bind to a different cadherin. In addition, some cadherins engage in heterophilic adhesion with other cadherins.

E-cadherin, one member of the cadherin superfamily, is expressed in epithelial cell types. Pathologically, if E-cadherin expression is lost in a tumor, the malignant cells
10 become invasive and the cancer metastasizes. Transfection of cancer cell lines with polynucleotides expressing E-cadherin has reversed cancer-associated changes by returning altered cell shapes to normal, restoring cells' adhesiveness to each other and to their substrate, decreasing the cell growth rate, and drastically reducing anchorage-independent cell growth. Thus, reintroducing E-cadherin expression reverts carcinomas
15 to a less advanced stage. It is likely that other cadherins have the same invasion suppressor role in carcinomas derived from other tissue types. Therefore, proteins of the present invention with cadherin activity, and polynucleotides of the present invention encoding such proteins, can be used to treat cancer. Introducing such proteins or polynucleotides into cancer cells can reduce or eliminate the cancerous changes observed
20 in these cells by providing normal cadherin expression.

Cancer cells have also been shown to express cadherins of a different tissue type than their origin, thus allowing these cells to invade and metastasize in a different tissue in the body. Proteins of the present invention with cadherin activity, and polynucleotides of the present invention encoding such proteins, can be substituted in these cells for the
25 inappropriately expressed cadherins, restoring normal cell adhesive properties and reducing or eliminating the tendency of the cells to metastasize.

Additionally, proteins of the present invention with cadherin activity, and polynucleotides of the present invention encoding such proteins, can be used to generate antibodies recognizing and binding to cadherins. Such antibodies can be used to block
30 the adhesion of inappropriately expressed tumor-cell cadherins, preventing the cells from forming a tumor elsewhere. Such an anti-cadherin antibody can also be used as a marker for the grade, pathological type, and prognosis of a cancer, i.e. the more progressed the cancer, the less cadherin expression there will be, and this decrease in cadherin expression can be detected by the use of a cadherin-binding antibody.

Fragments of proteins of the present invention with cadherin activity, preferably a polypeptide comprising a decapeptide of the cadherin recognition site, and polynucleotides of the present invention encoding such protein fragments, can also be used to block cadherin function by binding to cadherins and preventing them from binding in ways that produce undesirable effects. Additionally, fragments of proteins of the present invention with cadherin activity, preferably truncated soluble cadherin fragments which have been found to be stable in the circulation of cancer patients, and polynucleotides encoding such protein fragments, can be used to disturb proper cell-cell adhesion.

Assays for cadherin adhesive and invasive suppressor activity include, without limitation, those described in: Hortsch et al. J Biol Chem 270 (32): 18809-18817, 1995; Miyaki et al. Oncogene 11: 2547-2552, 1995; Ozawa et al. Cell 63: 1033-1038, 1990.

Tumor Inhibition Activity

In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may inhibit tumor growth directly or indirectly (such as, for example, via antibody-dependent cell-mediated cytotoxicity (ADCC)). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

Other Activities

A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s);

effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

ADMINISTRATION AND DOSING

A protein of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources) may be used in a pharmaceutical composition when combined with a pharmaceutically acceptable carrier. Such a composition may also contain (in addition to protein and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or compliment its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein of the invention, or to minimize side effects. Conversely, protein of the present invention may be included in formulations of the particular cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent.

A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical

compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithin, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent No. 4,235,871; U.S. Patent No. 4,501,728; U.S. Patent No. 4,837,028; and U.S. Patent No. 4,737,323, all of which are incorporated herein by reference.

As used herein, the term "therapeutically effective amount" means the total amount of each active component of the pharmaceutical composition or method that is sufficient to show a meaningful patient benefit, i.e., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, the term refers to that ingredient alone. When applied to a combination, the term refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein of the present invention is administered to a mammal having a condition to be treated. Protein of the present invention may be administered in accordance with the method of the invention either alone or in
5 combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other hematopoietic factors, protein of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other
10 hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

Administration of protein of the present invention used in the pharmaceutical
15 composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

When a therapeutically effective amount of protein of the present invention is
20 administered orally, protein of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein of the present invention, and preferably from about 25 to 90% protein of the present invention.
25 When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid
30 form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein of the present invention, and preferably from about 1 to 50% protein of the present invention.

When a therapeutically effective amount of protein of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein of the present

invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art.

10 The amount of protein of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein of the present invention with which to treat each individual patient. Initially, the attending physician

15 will administer low doses of protein of the present invention and observe the patient's response. Larger doses of protein of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 µg to about 100

20 mg (preferably about 0.1mg to about 10 mg, more preferably about 0.1 µg to about 1 mg) of protein of the present invention per kg body weight.

 The duration of intravenous therapy using the pharmaceutical composition of the present invention will vary, depending on the severity of the disease being treated and the condition and potential idiosyncratic response of each individual patient. It is

25 contemplated that the duration of each application of the protein of the present invention will be in the range of 12 to 24 hours of continuous intravenous administration. Ultimately the attending physician will decide on the appropriate duration of intravenous therapy using the pharmaceutical composition of the present invention.

 Protein of the invention may also be used to immunize animals to obtain

30 polyclonal and monoclonal antibodies which specifically react with the protein. As used herein, the term "antibody" includes without limitation a polyclonal antibody, a monoclonal antibody, a chimeric antibody, a single-chain antibody, a CDR-grafted antibody, a humanized antibody, or fragments thereof which bind to the indicated protein.

Such term also includes any other species derived from an antibody or antibody sequence which is capable of binding the indicated protein.

Antibodies to a particular protein can be produced by methods well known to those skilled in the art. For example, monoclonal antibodies can be produced by generation of
5 antibody-producing hybridomas in accordance with known methods (see for example, Goding, 1983, *Monoclonal antibodies: principles and practice*, Academic Press Inc., New York; and Yokoyama, 1992, "Production of Monoclonal Antibodies" in *Current Protocols in Immunology*, Unit 2.5, Greene Publishing Assoc. and John Wiley & Sons). Polyclonal sera and antibodies can be produced by inoculation of a mammalian subject with the
10 relevant protein or fragments thereof in accordance with known methods. Fragments of antibodies, receptors, or other reactive peptides can be produced from the corresponding antibodies by cleavage of and collection of the desired fragments in accordance with known methods (see for example, Goding, *supra*; and Andrew et al., 1992, "Fragmentation of Immunoglobulins" in *Current Protocols in Immunology*, Unit 2.8, Greene Publishing
15 Assoc. and John Wiley & Sons). Chimeric antibodies and single chain antibodies can also be produced in accordance with known recombinant methods (see for example, 5,169,939, 5,194,594, and 5,576,184). Humanized antibodies can also be made from corresponding murine antibodies in accordance with well known methods (see for example, U.S. Patent Nos. 5,530,101, 5,585,089, and 5,693,762). Additionally, human antibodies may be
20 produced in non-human animals such as mice that have been genetically altered to express human antibody molecules (see for example Fishwild *et al.*, 1996, *Nature Biotechnology* 14: 845-851; Mendez *et al.*, 1997, *Nature Genetics* 15: 146-156 (erratum *Nature Genetics* 16: 410); and U.S. Patents 5,877,397 and 5,625,126). Such antibodies may be obtained using either the entire protein or fragments thereof as an immunogen. The peptide
25 immunogens additionally may contain a cysteine residue at the carboxyl terminus, and are conjugated to a hapten such as keyhole limpet hemocyanin (KLH). Methods for synthesizing such peptides are known in the art, for example, as in R.P. Merrifield, J. Amer.Chem.Soc. 85, 2149-2154 (1963); J.L. Krstenansky, *et al.*, FEBS Lett. 211, 10 (1987).

Monoclonal antibodies binding to the protein of the invention may be useful
30 diagnostic agents for the immunodetection of the protein. Neutralizing monoclonal antibodies binding to the protein may also be useful therapeutics for both conditions associated with the protein and also in the treatment of some forms of cancer where

abnormal expression of the protein is involved. In the case of cancerous cells or leukemic cells, neutralizing monoclonal antibodies against the protein may be useful in detecting and preventing the metastatic spread of the cancerous cells, which may be mediated by the protein.

5 For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably
10 be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the
15 methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical
20 applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium
25 sulfate, tricalciumphosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxyapatite, bioglass, aluminates, or other
30 ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalciumphosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability.

Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions
5 from disassociating from the matrix.

A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropylmethylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of
10 carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt%, preferably 1-10 wt% based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to
15 provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells.

In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in
20 question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF- α and TGF- β), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to
25 humans, are desired patients for such treatment with proteins of the present invention.

The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, e.g., amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of
30 a wound, type of damaged tissue (e.g., bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect

the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such
5 polynucleotides can be introduced either *in vivo* or *ex vivo* into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA).

Cells may also be cultured *ex vivo* in the presence of proteins of the present
10 invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes.

Patent and literature references cited herein are incorporated by reference as if fully set forth.

What is claimed is:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:
 - (a) the nucleotide sequence of SEQ ID NO:1;
 - (b) the nucleotide sequence of SEQ ID NO:1 from nucleotide 29 to nucleotide 253;
 - (c) the nucleotide sequence of the full-length protein coding sequence of clone ya15_1 deposited under accession number ATCC 98650;
 - (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone ya15_1 deposited under accession number ATCC 98650;
 - (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:2;
 - (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2, the fragment comprising eight contiguous amino acids of SEQ ID NO:2;
 - (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
 - (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:1.
2. The polynucleotide of claim 1 wherein said polynucleotide is operably linked to at least one expression control sequence.
3. A host cell transformed with the polynucleotide of claim 2.
4. The host cell of claim 3, wherein said cell is a mammalian cell.
5. A process for producing a protein encoded by the polynucleotide of claim 2, which process comprises:
 - (a) growing a culture of a host cell transformed with the polynucleotide of claim 2 in a suitable culture medium; and

- (b) purifying said protein from the culture.
- 6. A protein produced according to the process of claim 5.
 - 7. An isolated polynucleotide encoding the protein of claim 6.
 - 8. The polynucleotide of claim 7, wherein the polynucleotide comprises the cDNA insert of clone ya15_1 deposited under accession number ATCC 98650.
 - 9. A protein comprising an amino acid sequence selected from the group consisting of:
 - (a) the amino acid sequence of SEQ ID NO:2;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:2, the fragment comprising eight contiguous amino acids of SEQ ID NO:2; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone ya15_1 deposited under accession number ATCC 98650;the protein being substantially free from other mammalian proteins.
 - 10. The protein of claim 9, wherein said protein comprises the amino acid sequence of SEQ ID NO:2.
 - 11. A composition comprising the protein of claim 9 and a pharmaceutically acceptable carrier.
 - 12. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:
 - (a) the nucleotide sequence of SEQ ID NO:3;
 - (b) the nucleotide sequence of SEQ ID NO:3 from nucleotide 151 to nucleotide 288;
 - (c) the nucleotide sequence of SEQ ID NO:3 from nucleotide 196 to nucleotide 288;
 - (d) the nucleotide sequence of the full-length protein coding sequence of clone ya24_1 deposited under accession number ATCC 98650;

- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone ya24_1 deposited under accession number ATCC 98650;
- (f) the nucleotide sequence of a mature protein coding sequence of clone ya24_1 deposited under accession number ATCC 98650;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone ya24_1 deposited under accession number ATCC 98650;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:4;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4, the fragment comprising eight contiguous amino acids of SEQ ID NO:4;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:3.

13. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:4;
- (b) a fragment of the amino acid sequence of SEQ ID NO:4, the fragment comprising eight contiguous amino acids of SEQ ID NO:4; and
- (c) the amino acid sequence encoded by the cDNA insert of clone ya24_1 deposited under accession number ATCC 98650;

the protein being substantially free from other mammalian proteins.

14. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:5;
- (b) the nucleotide sequence of SEQ ID NO:5 from nucleotide 615 to nucleotide 908;

- (c) the nucleotide sequence of SEQ ID NO:5 from nucleotide 774 to nucleotide 908;
 - (d) the nucleotide sequence of the full-length protein coding sequence of clone yb42_1 deposited under accession number ATCC 98650;
 - (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yb42_1 deposited under accession number ATCC 98650;
 - (f) the nucleotide sequence of a mature protein coding sequence of clone yb42_1 deposited under accession number ATCC 98650;
 - (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone yb42_1 deposited under accession number ATCC 98650;
 - (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:6;
 - (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6, the fragment comprising eight contiguous amino acids of SEQ ID NO:6;
 - (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
 - (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:5.
15. A protein comprising an amino acid sequence selected from the group consisting of:
- (a) the amino acid sequence of SEQ ID NO:6;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:6, the fragment comprising eight contiguous amino acids of SEQ ID NO:6; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone yb42_1 deposited under accession number ATCC 98650;
- the protein being substantially free from other mammalian proteins.

16. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:7;
- (b) the nucleotide sequence of SEQ ID NO:7 from nucleotide 1203 to nucleotide 2327;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone yc9_1 deposited under accession number ATCC 98650;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yc9_1 deposited under accession number ATCC 98650;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:8;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8, the fragment comprising eight contiguous amino acids of SEQ ID NO:8;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:7.

17. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:8;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:8, the fragment comprising eight contiguous amino acids of SEQ ID NO:8; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone yc9_1 deposited under accession number ATCC 98650;
- the protein being substantially free from other mammalian proteins.

18. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:9;
- (b) the nucleotide sequence of SEQ ID NO:9 from nucleotide 230 to nucleotide 823;

- (c) the nucleotide sequence of SEQ ID NO:9 from nucleotide 584 to nucleotide 823;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone yc19_1 deposited under accession number ATCC 98650;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yc19_1 deposited under accession number ATCC 98650;
- (f) the nucleotide sequence of a mature protein coding sequence of clone yc19_1 deposited under accession number ATCC 98650;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone yc19_1 deposited under accession number ATCC 98650;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:10;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10, the fragment comprising eight contiguous amino acids of SEQ ID NO:10;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:9.

19. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:10;
- (b) a fragment of the amino acid sequence of SEQ ID NO:10, the fragment comprising eight contiguous amino acids of SEQ ID NO:10; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yc19_1 deposited under accession number ATCC 98650;

the protein being substantially free from other mammalian proteins.

20. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:11;
- (b) the nucleotide sequence of SEQ ID NO:11 from nucleotide 292 to nucleotide 534;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone yc20_1 deposited under accession number ATCC 98650;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yc20_1 deposited under accession number ATCC 98650;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:12;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12, the fragment comprising eight contiguous amino acids of SEQ ID NO:12;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:11.

21. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:12;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:12, the fragment comprising eight contiguous amino acids of SEQ ID NO:12; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone yc20_1 deposited under accession number ATCC 98650;
- the protein being substantially free from other mammalian proteins.

22. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:13;
- (b) the nucleotide sequence of SEQ ID NO:13 from nucleotide 45 to nucleotide 590;

- (c) the nucleotide sequence of SEQ ID NO:13 from nucleotide 126 to nucleotide 590;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone ya9_1 deposited under accession number ATCC 98724;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone ya9_1 deposited under accession number ATCC 98724;
- (f) the nucleotide sequence of a mature protein coding sequence of clone ya9_1 deposited under accession number ATCC 98724;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone ya9_1 deposited under accession number ATCC 98724;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:14;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14, the fragment comprising eight contiguous amino acids of SEQ ID NO:14;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:13.

23. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:14;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:14, the fragment comprising eight contiguous amino acids of SEQ ID NO:14; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone ya9_1 deposited under accession number ATCC 98724;
- the protein being substantially free from other mammalian proteins.

24. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:15;
- (b) the nucleotide sequence of SEQ ID NO:15 from nucleotide 194 to nucleotide 466;
- (c) the nucleotide sequence of SEQ ID NO:15 from nucleotide 338 to nucleotide 466;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone ya11_1 deposited under accession number ATCC 98724;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone ya11_1 deposited under accession number ATCC 98724;
- (f) the nucleotide sequence of a mature protein coding sequence of clone ya11_1 deposited under accession number ATCC 98724;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone ya11_1 deposited under accession number ATCC 98724;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:16;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16, the fragment comprising eight contiguous amino acids of SEQ ID NO:16;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:15.

25. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:16;
- (b) a fragment of the amino acid sequence of SEQ ID NO:16, the fragment comprising eight contiguous amino acids of SEQ ID NO:16; and
- (c) the amino acid sequence encoded by the cDNA insert of clone ya11_1 deposited under accession number ATCC 98724;

the protein being substantially free from other mammalian proteins.

26. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:17;
- (b) the nucleotide sequence of SEQ ID NO:17 from nucleotide 15 to nucleotide 233;
- (c) the nucleotide sequence of SEQ ID NO:17 from nucleotide 174 to nucleotide 233;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone ya28_1 deposited under accession number ATCC 98724;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone ya28_1 deposited under accession number ATCC 98724;
- (f) the nucleotide sequence of a mature protein coding sequence of clone ya28_1 deposited under accession number ATCC 98724;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone ya28_1 deposited under accession number ATCC 98724;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:18;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18, the fragment comprising eight contiguous amino acids of SEQ ID NO:18;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:17.

27. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:18;
- (b) a fragment of the amino acid sequence of SEQ ID NO:18, the fragment comprising eight contiguous amino acids of SEQ ID NO:18; and

(c) the amino acid sequence encoded by the cDNA insert of clone ya28_1 deposited under accession number ATCC 98724; the protein being substantially free from other mammalian proteins.

28. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:19;
- (b) the nucleotide sequence of SEQ ID NO:19 from nucleotide 102 to nucleotide 461;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone yb81_1 deposited under accession number ATCC 98724;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yb81_1 deposited under accession number ATCC 98724;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:20;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20, the fragment comprising eight contiguous amino acids of SEQ ID NO:20;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:19.

29. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:20;
- (b) a fragment of the amino acid sequence of SEQ ID NO:20, the fragment comprising eight contiguous amino acids of SEQ ID NO:20; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yb81_1 deposited under accession number ATCC 98724; the protein being substantially free from other mammalian proteins.

30. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:21;
- (b) the nucleotide sequence of SEQ ID NO:21 from nucleotide 170 to nucleotide 2968;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone yc14_1 deposited under accession number ATCC 98724;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yc14_1 deposited under accession number ATCC 98724;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:22;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22, the fragment comprising eight contiguous amino acids of SEQ ID NO:22;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:21.

31. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:22;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:22, the fragment comprising eight contiguous amino acids of SEQ ID NO:22; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone yc14_1 deposited under accession number ATCC 98724;
- the protein being substantially free from other mammalian proteins.

32. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:23;
 - (b) the nucleotide sequence of SEQ ID NO:23 from nucleotide 82 to nucleotide 729;
 - (c) the nucleotide sequence of the full-length protein coding sequence of clone yc24_1 deposited under accession number ATCC 98755;
 - (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yc24_1 deposited under accession number ATCC 98755;
 - (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:24;
 - (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24, the fragment comprising eight contiguous amino acids of SEQ ID NO:24;
 - (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
 - (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:23.
33. A protein comprising an amino acid sequence selected from the group consisting of:
- (a) the amino acid sequence of SEQ ID NO:24;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:24, the fragment comprising eight contiguous amino acids of SEQ ID NO:24; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone yc24_1 deposited under accession number ATCC 98755;
- the protein being substantially free from other mammalian proteins.
34. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:
- (a) the nucleotide sequence of SEQ ID NO:25;
 - (b) the nucleotide sequence of SEQ ID NO:25 from nucleotide 7 to nucleotide 951;

- (c) the nucleotide sequence of SEQ ID NO:25 from nucleotide 61 to nucleotide 951;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone yc25_1 deposited under accession number ATCC 98755;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yc25_1 deposited under accession number ATCC 98755;
- (f) the nucleotide sequence of a mature protein coding sequence of clone yc25_1 deposited under accession number ATCC 98755;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone yc25_1 deposited under accession number ATCC 98755;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:26;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26, the fragment comprising eight contiguous amino acids of SEQ ID NO:26;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:25.

35. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:26;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:26, the fragment comprising eight contiguous amino acids of SEQ ID NO:26; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone yc25_1 deposited under accession number ATCC 98755;
- the protein being substantially free from other mammalian proteins.

36. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:27;
- (b) the nucleotide sequence of SEQ ID NO:27 from nucleotide 157 to nucleotide 1083;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone ye2_1 deposited under accession number ATCC 98755;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone ye2_1 deposited under accession number ATCC 98755;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:28;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28, the fragment comprising eight contiguous amino acids of SEQ ID NO:28;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:27.

37. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:28;
- (b) a fragment of the amino acid sequence of SEQ ID NO:28, the fragment comprising eight contiguous amino acids of SEQ ID NO:28; and
- (c) the amino acid sequence encoded by the cDNA insert of clone ye2_1 deposited under accession number ATCC 98755;

the protein being substantially free from other mammalian proteins.

38. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:29;
- (b) the nucleotide sequence of SEQ ID NO:29 from nucleotide 39 to nucleotide 473;

- (c) the nucleotide sequence of the full-length protein coding sequence of clone ya65_1 deposited under accession number ATCC 98834;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone ya65_1 deposited under accession number ATCC 98834;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:30;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30, the fragment comprising eight contiguous amino acids of SEQ ID NO:30;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:29.

39. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:30;
- (b) a fragment of the amino acid sequence of SEQ ID NO:30, the fragment comprising eight contiguous amino acids of SEQ ID NO:30; and
- (c) the amino acid sequence encoded by the cDNA insert of clone ya65_1 deposited under accession number ATCC 98834;

the protein being substantially free from other mammalian proteins.

40. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:31;
- (b) the nucleotide sequence of SEQ ID NO:31 from nucleotide 664 to nucleotide 903;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone yb60_1 deposited under accession number ATCC 98834;

- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yb60_1 deposited under accession number ATCC 98834;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:32;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32, the fragment comprising eight contiguous amino acids of SEQ ID NO:32;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:31.

41. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:32;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:32, the fragment comprising eight contiguous amino acids of SEQ ID NO:32; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone yb60_1 deposited under accession number ATCC 98834;
- the protein being substantially free from other mammalian proteins.

42. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:33;
- (b) the nucleotide sequence of SEQ ID NO:33 from nucleotide 88 to nucleotide 447;
- (c) the nucleotide sequence of SEQ ID NO:33 from nucleotide 427 to nucleotide 447;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone yb139_1 deposited under accession number ATCC 98834;

- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yb139_1 deposited under accession number ATCC 98834;
- (f) the nucleotide sequence of a mature protein coding sequence of clone yb139_1 deposited under accession number ATCC 98834;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone yb139_1 deposited under accession number ATCC 98834;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:34;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34, the fragment comprising eight contiguous amino acids of SEQ ID NO:34;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:33.

43. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:34;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:34, the fragment comprising eight contiguous amino acids of SEQ ID NO:34; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone yb139_1 deposited under accession number ATCC 98834;.
- the protein being substantially free from other mammalian proteins.

44. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:35;
- (b) the nucleotide sequence of SEQ ID NO:35 from nucleotide 93 to nucleotide 1481;

- (c) the nucleotide sequence of the full-length protein coding sequence of clone yc29_1 deposited under accession number ATCC 98834;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yc29_1 deposited under accession number ATCC 98834;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:36;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36, the fragment comprising eight contiguous amino acids of SEQ ID NO:36;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:35.

45. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:36;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:36, the fragment comprising eight contiguous amino acids of SEQ ID NO:36; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone yc29_1 deposited under accession number ATCC 98834;
- the protein being substantially free from other mammalian proteins.

46. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:37;
- (b) the nucleotide sequence of SEQ ID NO:37 from nucleotide 482 to nucleotide 751;
- (c) the nucleotide sequence of SEQ ID NO:37 from nucleotide 611 to nucleotide 751;

- (d) the nucleotide sequence of the full-length protein coding sequence of clone yc40_1 deposited under accession number ATCC 98834;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yc40_1 deposited under accession number ATCC 98834;
- (f) the nucleotide sequence of a mature protein coding sequence of clone yc40_1 deposited under accession number ATCC 98834;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone yc40_1 deposited under accession number ATCC 98834;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:38;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38, the fragment comprising eight contiguous amino acids of SEQ ID NO:38;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:37.

47. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:38;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:38, the fragment comprising eight contiguous amino acids of SEQ ID NO:38; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone yc40_1 deposited under accession number ATCC 98834;
- the protein being substantially free from other mammalian proteins.

48. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:39;

- (b) the nucleotide sequence of SEQ ID NO:39 from nucleotide 179 to nucleotide 601;
- (c) the nucleotide sequence of SEQ ID NO:39 from nucleotide 356 to nucleotide 601;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone yd10_1 deposited under accession number ATCC 98834;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yd10_1 deposited under accession number ATCC 98834;
- (f) the nucleotide sequence of a mature protein coding sequence of clone yd10_1 deposited under accession number ATCC 98834;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone yd10_1 deposited under accession number ATCC 98834;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:40;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40, the fragment comprising eight contiguous amino acids of SEQ ID NO:40;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:39.

49. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:40;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:40, the fragment comprising eight contiguous amino acids of SEQ ID NO:40; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone yd10_1 deposited under accession number ATCC 98834;
- the protein being substantially free from other mammalian proteins.

50. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:41;
- (b) the nucleotide sequence of SEQ ID NO:41 from nucleotide 324 to nucleotide 1559;
- (c) the nucleotide sequence of SEQ ID NO:41 from nucleotide 387 to nucleotide 1559;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone yf5_1 deposited under accession number ATCC 98834;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yf5_1 deposited under accession number ATCC 98834;
- (f) the nucleotide sequence of a mature protein coding sequence of clone yf5_1 deposited under accession number ATCC 98834;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone yf5_1 deposited under accession number ATCC 98834;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:42;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42, the fragment comprising eight contiguous amino acids of SEQ ID NO:42;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:41.

51. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:42;
- (b) a fragment of the amino acid sequence of SEQ ID NO:42, the fragment comprising eight contiguous amino acids of SEQ ID NO:42; and

(c) the amino acid sequence encoded by the cDNA insert of clone yf5_1 deposited under accession number ATCC 98834;
the protein being substantially free from other mammalian proteins.

52. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:43;
- (b) the nucleotide sequence of SEQ ID NO:43 from nucleotide 257 to nucleotide 649;
- (c) the nucleotide sequence of SEQ ID NO:43 from nucleotide 335 to nucleotide 649;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone ya67_1 deposited under accession number ATCC 98864;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone ya67_1 deposited under accession number ATCC 98864;
- (f) the nucleotide sequence of a mature protein coding sequence of clone ya67_1 deposited under accession number ATCC 98864;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone ya67_1 deposited under accession number ATCC 98864;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:44;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44, the fragment comprising eight contiguous amino acids of SEQ ID NO:44;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:43.

53. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:44;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:44, the fragment comprising eight contiguous amino acids of SEQ ID NO:44; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone ya67_1 deposited under accession number ATCC 98864;
- the protein being substantially free from other mammalian proteins.

54. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:45;
- (b) the nucleotide sequence of SEQ ID NO:45 from nucleotide 89 to nucleotide 787;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone ya70_1 deposited under accession number ATCC 98864;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone ya70_1 deposited under accession number ATCC 98864;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:46;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46, the fragment comprising eight contiguous amino acids of SEQ ID NO:46;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:45.

55. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:46;
- (b) a fragment of the amino acid sequence of SEQ ID NO:46, the fragment comprising eight contiguous amino acids of SEQ ID NO:46; and

(c) the amino acid sequence encoded by the cDNA insert of clone ya70_1 deposited under accession number ATCC 98864; the protein being substantially free from other mammalian proteins.

56. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:47;
- (b) the nucleotide sequence of SEQ ID NO:47 from nucleotide 1017 to nucleotide 1265;
- (c) the nucleotide sequence of SEQ ID NO:47 from nucleotide 1068 to nucleotide 1265;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone yb51_1 deposited under accession number ATCC 98864;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yb51_1 deposited under accession number ATCC 98864;
- (f) the nucleotide sequence of a mature protein coding sequence of clone yb51_1 deposited under accession number ATCC 98864;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone yb51_1 deposited under accession number ATCC 98864;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:48;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48, the fragment comprising eight contiguous amino acids of SEQ ID NO:48;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:47.

57. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:48;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:48, the fragment comprising eight contiguous amino acids of SEQ ID NO:48; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone yb51_1 deposited under accession number ATCC 98864;
- the protein being substantially free from other mammalian proteins.

58. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:49;
- (b) the nucleotide sequence of SEQ ID NO:49 from nucleotide 13 to nucleotide 306;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone yb101_1 deposited under accession number ATCC 98864;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yb101_1 deposited under accession number ATCC 98864;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:50;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50, the fragment comprising eight contiguous amino acids of SEQ ID NO:50;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:49.

59. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:50;
- (b) a fragment of the amino acid sequence of SEQ ID NO:50, the fragment comprising eight contiguous amino acids of SEQ ID NO:50; and

(c) the amino acid sequence encoded by the cDNA insert of clone yb101_1 deposited under accession number ATCC 98864;
the protein being substantially free from other mammalian proteins.

60. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:51;
- (b) the nucleotide sequence of SEQ ID NO:51 from nucleotide 284 to nucleotide 706;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone yb124_1 deposited under accession number ATCC 98864;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yb124_1 deposited under accession number ATCC 98864;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:52;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52, the fragment comprising eight contiguous amino acids of SEQ ID NO:52;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:51.

61. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:52;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:52, the fragment comprising eight contiguous amino acids of SEQ ID NO:52; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone yb124_1 deposited under accession number ATCC 98864;
- the protein being substantially free from other mammalian proteins.

62. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:53;
- (b) the nucleotide sequence of SEQ ID NO:53 from nucleotide 1106 to nucleotide 1447;
- (c) the nucleotide sequence of SEQ ID NO:53 from nucleotide 1187 to nucleotide 1447;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone yb125_1 deposited under accession number ATCC 98864;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yb125_1 deposited under accession number ATCC 98864;
- (f) the nucleotide sequence of a mature protein coding sequence of clone yb125_1 deposited under accession number ATCC 98864;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone yb125_1 deposited under accession number ATCC 98864;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:54;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54, the fragment comprising eight contiguous amino acids of SEQ ID NO:54;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:53.

63. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:54;
- (b) a fragment of the amino acid sequence of SEQ ID NO:54, the fragment comprising eight contiguous amino acids of SEQ ID NO:54; and

(c) the amino acid sequence encoded by the cDNA insert of clone yb125_1 deposited under accession number ATCC 98864; the protein being substantially free from other mammalian proteins.

64. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:55;
- (b) the nucleotide sequence of SEQ ID NO:55 from nucleotide 28 to nucleotide 417;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone yb179_1 deposited under accession number ATCC 98864;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yb179_1 deposited under accession number ATCC 98864;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:56;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56, the fragment comprising eight contiguous amino acids of SEQ ID NO:56;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:55.

65. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:56;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:56, the fragment comprising eight contiguous amino acids of SEQ ID NO:56; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone yb179_1 deposited under accession number ATCC 98864;
- the protein being substantially free from other mammalian proteins.

66. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:57;
- (b) the nucleotide sequence of SEQ ID NO:57 from nucleotide 56 to nucleotide 1084;
- (c) the nucleotide sequence of SEQ ID NO:57 from nucleotide 107 to nucleotide 1084;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone yc48_1 deposited under accession number ATCC 98864;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yc48_1 deposited under accession number ATCC 98864;
- (f) the nucleotide sequence of a mature protein coding sequence of clone yc48_1 deposited under accession number ATCC 98864;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone yc48_1 deposited under accession number ATCC 98864;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:58;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58, the fragment comprising eight contiguous amino acids of SEQ ID NO:58;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:57.

67. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:58;
- (b) a fragment of the amino acid sequence of SEQ ID NO:58, the fragment comprising eight contiguous amino acids of SEQ ID NO:58; and

(c) the amino acid sequence encoded by the cDNA insert of clone yc48_1 deposited under accession number ATCC 98864; the protein being substantially free from other mammalian proteins.

68. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:59;
- (b) the nucleotide sequence of SEQ ID NO:59 from nucleotide 373 to nucleotide 660;
- (c) the nucleotide sequence of SEQ ID NO:59 from nucleotide 436 to nucleotide 660;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone ye21_1 deposited under accession number ATCC 98864;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone ye21_1 deposited under accession number ATCC 98864;
- (f) the nucleotide sequence of a mature protein coding sequence of clone ye21_1 deposited under accession number ATCC 98864;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone ye21_1 deposited under accession number ATCC 98864;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:60;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60, the fragment comprising eight contiguous amino acids of SEQ ID NO:60;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:59.

69. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:60;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:60, the fragment comprising eight contiguous amino acids of SEQ ID NO:60; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone ye21_1 deposited under accession number ATCC 98864;
- the protein being substantially free from other mammalian proteins.

70. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:61;
- (b) the nucleotide sequence of SEQ ID NO:61 from nucleotide 119 to nucleotide 466;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone ye22_1 deposited under accession number ATCC 98864;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone ye22_1 deposited under accession number ATCC 98864;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:62;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62, the fragment comprising eight contiguous amino acids of SEQ ID NO:62;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:61.

71. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:62;
- (b) a fragment of the amino acid sequence of SEQ ID NO:62, the fragment comprising eight contiguous amino acids of SEQ ID NO:62; and

(c) the amino acid sequence encoded by the cDNA insert of clone ye22_1 deposited under accession number ATCC 98864; the protein being substantially free from other mammalian proteins.

72. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:63;
- (b) the nucleotide sequence of SEQ ID NO:63 from nucleotide 1212 to nucleotide 1502;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone ye39_1 deposited under accession number ATCC 98861;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone ye39_1 deposited under accession number ATCC 98861;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:64;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64, the fragment comprising eight contiguous amino acids of SEQ ID NO:64;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:63.

73. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:64;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:64, the fragment comprising eight contiguous amino acids of SEQ ID NO:64; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone ye39_1 deposited under accession number ATCC 98861;
- the protein being substantially free from other mammalian proteins.